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New Insights on the Peopling of the New World: Analysis of Migration Waves and Ancestral Areas of the First Americans

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To the Graduate Council:

I am submitting herewith a dissertation written by Barbara Kathleen Alsup entitled "New Insights on the Peopling of the New World: Analysis of Migration Waves and Ancestral Areas of the First Americans." I have examined the final electronic copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Anthropology.

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New Insights on the Peopling of the New World: Analysis of Migration Waves and Ancestral Areas of the First Americans

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Abstract

There is much debate regarding the ancestral area(s) and migration patterns of the first migrants into the Americas, referred to here as Paleoamericans. Using craniometric data of a comprehensive sample of Paleoamericans, Archaic Americans and modern, worldwide populations, various statistical analyses were conducted to further investigate these research questions, such as principal component analysis, Mahalanobis squared distance matrices and matrix permutation and design matrix analysis.

Most results indicate that the Single Wave model for movement into the New World is best supported by this data. This finding is among the first in providing craniometric support for a single wave into the New World, which corresponds with findings in genetic research.

A definitive interpretation of ancestral area(s) of the Paleoamericans is not provided by these results. The evidence leans towards either southeast Asia/Pacific Rim or eastern Asia as the ancestral area for all geographic groupings of Paleoamericans. Additionally, there are consistent phenotypic connections between the North American Paleoamericans and modern, European populations as well as between South American Paleoamericans and modern, African populations. Whether this represents a true genotypic connection between these areas is dependent on additional research in cranial plasticity and modes of evolution within the Americas.

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Chapter One: Introduction

This dissertation seeks to explore unanswered, yet previously researched, questions surrounding the earliest migrants into the New World (North, Central and South America) during the Late Pleistocene and Early Holocene eras. These first migrants will be referred to throughout this dissertation as Paleoamericans. This term is utilized, rather than the more traditional term, Paleoindian, to refrain from implying that these earliest individuals were or were not ancestral to modern Native American populations (Powell and Neves, 1999). In particular, possible ancestral area(s) of the Paleoamericans, as well as previously proposed migration scenarios and waves throughout the Americas, are re-evaluated.

There are numerous anthropological means by which to explore these research areas, such as archaeology, linguistics and genetics. Possible ancestral areas and migration scenarios will be evaluated using a comprehensive craniometric data set. Model-free methods, such as principal component analysis, group descriptive statistics and Mahalanobis squared distance matrices, are used to evaluate both questions. Additionally, model-bound methods are used to investigate the associations between biological distance matrices and various design matrices, reflecting previously proposed ancestral areas and migration scenarios. These methods directly incorporate theoretical models of population structure. This is unlike model-free statistical methods that make no assumptions regarding the causes of phenotypic similarity between

populations (Relethford and Lees, 1982). Although it has been argued that model-bound approaches in anthropology are poorly developed (Konigsberg and Buikstra, 1995), there has been a movement to improve these methods and understand the caveats of model-bound statistical methods. Thus, this methodology has experienced a surge in Paleoamerican research (de Azevedo et al., 2011; Gonzalez-Jose et al., 2001; Hubbe et al., 2010).

The first hypothesis for this research is that there are numerous possible ancestral areas for the Paleoamericans, but the strongest phenotypic connections will be focused in southeast Asian and Pacific Rim populations. This hypothesis was developed because craniometric data is utilized here, and the best prior evidence for a southeast Asian and/or Pacific Rim ancestral area comes from morphological research (Jantz and Owsley, 2005; Neves et al., 2007; Steele and Powell, 2002). Secondly, in regards to migration scenarios, this analysis may provide evidence that the Two Component model provides the best explanation of movement into the New World, similar to that found in various publications utilizing craniometrics (Neves and Pucciarelli, 1991; Pucciarelli et al., 2003; Powell and Neves, 1999). This model will be discussed in Chapter Three.

The first chapter serves as a brief introduction to the questions being addressed as well as generalized methods utilized in this dissertation. Chapter Two is a review of the literature concerning craniometrics, specifically its use in biodistance analyses. Chapter Three explores previous ideas pertaining to the peopling of the New World with a focus on earlier research regarding ancestral regions of Paleoamericans as well as migration scenarios. Additionally, chapter

Three delves into migration theory and models in anthropological research, specifically in regards to movements into unoccupied or sparsely occupied areas. Chapter Four outlines the materials used in this dissertation, including in-depth descriptions of the Paleoamerican sample, sample sizes for all populations and associated dates or archaeological time periods for each site. Chapter Five explains the methodology utilized in the analysis of possible ancestral areas and migration scenarios. Chapter Six introduces the results and provides discussion for the model-free and model-bound statistical methods. Chapter Seven supplies concluding remarks and presents future areas of research.

While this dissertation is not meant to advocate or argue against components of the Native American Graves Protection and Repatriation Act (NAGPRA), it is certainly affected by the actions of museums, scientists and Native American groups because of this legislation. This is particularly true in the availability of previously discovered Paleoamerican skeletal remains for scientific study. It is important to understand what NAGPRA is, why it was enacted, how it is carried out by museums, scientists, Native American groups and the US government, and controversies surrounding misinterpretations and miscommunications of the law, particularly in regards to access to skeletal remains that have been deemed “culturally unidentifiable.” As this is a United States law, it only pertains to remains found and housed in the US, and thus, the remains of the earliest Americans found in Central and South America and Canada are not affected by the NAGPRA. These countries have different laws and ideals in regards to repatriation and reburial of past remains.

There were several precursors to the NAGPRA but the most pertinent was enacted a year before: the National Museum of the American Indian Act (NMAIA). There are countless similarities between the two, but the biggest difference is that the NMAIA is specific to the National Museum of the American Indian (part of the Smithsonian Institute), while the NAGPRA applies to all government agencies and institutions that receive federal funds (Ousley et al., 2005). The NMAIA served as the foundation for the nationwide NAGPRA legislation (Inouye, 1990).

The 101st US Congress passed the NAGPRA (Public Law 101-601) on November 16, 1990. The act was developed through the combined efforts of the Native American Rights Fund, American Association of Physical Anthropologists, Society for American Archaeology and National Congress of American Indians (Lovis et al., 2004). The primary purpose of the NAGPRA was to establish more standardized procedures for determining affiliation and ownership of Native American remains and cultural materials found on tribal or federal lands after November 16, 1990. In addition, the NAGPRA sets guidelines for the determination of repatriation of any Native American remains or cultural materials already in the possession or housed in museums and federal agencies (Ousley et al., 2005). This meant that all federally funded museums or agencies had to complete a detailed inventory of all Native American skeletal remains and associated cultural objects. In addition, these repositories had to identify their cultural affiliation and geographic origin “to the extent possible based on information possessed” by the agency or museum (25 U.S.C.3003(a)).

As mentioned above, cultural affiliation is to be determined by federal agencies and museums. However, cultural affiliation can be hard to define. The NAGPRA defines it as “a relationship of shared group identity which can be reasonably traced historically and prehistorically between a present day [federally recognized] Indian tribe or Native Hawaiian organization and an identifiable earlier group” (25 U.S.C. 3001(2)). Additionally, these regulations explain that a relationship of descent must be established between the earlier group and the present-day tribe (43 CFR 10.14 (c) (3)). Cultural affiliation can be much easier to determine for historical remains. Oral histories or historical maps can help identify an ancestor-descendant relationship. For human remains predating written histories, it can be considerably more difficult to determine cultural affiliation, and this is where the knowledge and resources of archaeologists and biological anthropologists become very important assets.

The impact of the NAGPRA law on physical anthropologist and archaeologists has been great, particularly those studying culturally unidentifiable and/or prehistoric human remains or artifacts. Affiliated remains are almost always unavailable for study and many of these are already repatriated or reburied. Affiliated remains awaiting disposition decisions by Native Americans, but are still in the possession of museums or other repositories, are also generally unavailable for study, unless permission is obtained from the affiliated Native American group. The NAGPRA has greatly changed museum policies, with many greatly or completely restricting access to prehistoric human remains

(Ousley et al., 2005). However, it is important to note that the NAGPRA does *not* prohibit research on human remains (Stevenson, 1998).

As can be imagined, it is often difficult to determine cultural affiliation for Paleoamerican skeletal remains. However, this has not hindered the claims on the remains by Native American tribes or the premature repatriation of some remains before cultural affiliation has been soundly established. Perhaps the most high-profile case involves the remains discovered in Kennewick, Washington, often referred to as Kennewick Man. The NAGPRA claims on the skeletal material and associated cultural artifacts began almost immediately after the announcement of the discovery. The US Army Corps of Engineers (COE) decided that all materials would be turned over to a coalition of five Native American tribes in the area. These tribes include the Confederated Tribes of the Umatilla Indian Reservation, the Nez Perce tribe, the Corville tribe, the Yakima nation and Wanapum bands (Powell, 2005).

After the announcement by the US Army COE, scientists quickly protested and contended that there should be more analysis and consideration before these important remains were repatriated or reburied (Thomas, 2000). A group of scientists (R. Bonnichsen, D. Owsley, D. Stanford, D.G. Steele, R. Jantz, G. Gill, C.L. Brace and C.V. Haynes Jr.) filed an injunction to stop the repatriation of the Kennewick remains. Their main argument was that proceedings were not legal under the NAGPRA. This case began on October 16, 1996 (Shafer and Stang, 1996).

A year later, the US Army COE admitted that they had allowed members of the tribal coalition access to the Kennewick remains, in the form of performing religious ceremonies around the remains. An additional controversial event occurred in April 1998 when the COE buried the Kennewick discovery site with several tons of gravel and rock in order to protect this embankment from erosion. This makes further excavation around the Kennewick discovery site impossible. The COE eventually relinquished control of the decision concerning the skeletal remains' NAGPRA status. The courts decided that the Kennewick skeleton was not Native American under the NAGPRA law, which was also upheld by the 9th circuit, the COE became responsible for curating it under ARPA. The skeletal material is currently under limited availability for study (government-appointed) and is curated by the Burke Museum at the University of Washington at Seattle. Therefore, this author was not allowed access to the remains, but fortunately, previous access was possible and these measurements were used. This is just one example of the effects of the NAGPRA on the availability of skeletal remains either due to limited access or repatriation and/or reburial.

Chapter Two: Biodistance Analysis and Craniometrics

Introduction to biological distance analysis

One of the cornerstones of biological anthropology is describing and quantifying levels of genotypic similarity and dissimilarity through analysis of various phenotypic traits between human groups or populations. This type of research has enjoyed considerable success in historical studies (Larsen, 1997). Many methods used in historical studies are being used with varying levels of success with prehistoric "populations." Biological distance, biodistance, methods are the most common way of comparing phenotypic and genotypic similarities and dissimilarities between populations or individuals in biological anthropology.

Biodistance analysis can include both skeletal and molecular data, and ideally both types of data should produce similar results. This dissertation, as well as a majority of biodistance research regarding the peopling of the New World, will focus on biodistance analysis utilizing skeletal data. Here the term, "biodistance," refers to the measurement or observation of skeletal metric or nonmetric landmarks and the interpretation of relatedness or difference between populations (Buikstra et al., 1990). The most important assumption of biodistance analysis is that populations sharing more skeletal characteristics are more closely related than populations that have more differences. This assumption is often re-analyzed, particularly since it is known there are factors, such as genetic drift and climatic and functional adaptations that can affect phenotypes other than genotypes. Even with this knowledge, there seems to be a general consensus

that the aforementioned assumption is a fair one (Konigsberg and Ousley, 1995; Relethford et al., 1997).

Even though biodistance analysis may appear to be simplistic (for example, if two populations share twenty traits, they must be more related than two populations who share fifteen traits), it can be complex, particularly in regards to identifying meaningful patterns of biological variation (Nelson, 1992). Two of the most important issues in all biodistance studies are differences between individuals or populations in temporal and geographic distributions. There is much debate as to how or whether one should attempt to compare populations that are variable in terms of time and/or geography. However, it is a necessity for most prehistoric research, especially when focusing on the peopling of the New World. Thus, special care must be taken to account for or acknowledge these differences. This will be discussed in more detail in the methodology chapter (Chapter 5) of this dissertation.

Most biodistance studies consider multiple traits simultaneously through multivariate statistical analysis. If only one, or even a few, traits are used to compare populations, this may provide an inaccurate picture of relatedness due to low heritability of the traits under investigation. Thus, it is often a goal to use as many traits as possible in analysis; however, this is difficult due to the often-fragmentary nature of prehistoric skeletal remains. Examples of commonly used statistical methods in biodistance analysis include principal components analysis, discriminant function analysis, cluster analysis, multidimensional scaling and multivariate Mahalanobis distances (Larsen, 1997). Recently, various model-

bound methods, such as F_{ST} and design matrices, have been employed in biodistance analysis.

Heritability of Cranial Traits

As cranial metrics are the data utilized in this dissertation, it is important to consider the role of heritability and the multifactorial nature of cranial traits. All skeletal traits are influenced by genetic, as well as epigenetic, developmental, climatic and functional factors (Havarti and Weaver, 2006). Thus, neither metric nor nonmetric characteristics bear a complete one-to-one correspondence with an individual's genome. This has led to different types of heritability estimates for skeletal traits to better understand the relationship between genotype and phenotype.

There are two main types of heritability estimates: broad sense and narrow sense. Broad sense heritability is calculated by dividing total genotypic variance by total phenotypic variance (Hartl and Clark, 1997). These estimates are used to broadly argue whether or not genetic factors influence a trait in any way. A similar, but more commonly used, estimation, narrow sense heritability, is an approximation of the variation in a phenotypic trait for a population that can be attributed to additive genetic components. This estimation ranges from zero to one and can only be attributed to genetic components (Carson, 2006). Thus, the narrow sense heritability gives the researcher a better idea of the degree to which a trait is inherited. Consequently, if the narrow sense heritability is significant, then so to will the broad sense heritability (Kohn, 1991). Different traits on the skeleton can have widely varying heritability estimates. Even

neighboring features, i.e. different portions of the cranium, are different in their heritabilities (Carson, 2006).

A common practice in biodistance analyses utilizing craniometric data is to average previously reported narrow-sense heritabilities (a standard figure is h^2 = 0.55) or to simply assume that phenotypic and genotypic correlation are proportional. This can be problematic because recently published heritabilities are as low as 0.22 and are variable for different portions of the skull. Carson (2006) published narrow sense heritabilities for facial dimensions averaging h^2 = 0.268 and h^2 = 0.304 for neurocranial measures. The author argues that averaging this variability will not produce an accurate characterization of the heritability of the cranium as a whole, and this research, among others (Devor, 1987; Havarti and Weaver, 2006; van Vark et al., 2003), shows that caution needs to be taken when interpreting similar craniometric traits as an indicator of population relationships.

However, these heritability estimates have been used for decades and consistent results have been reported. Additionally, like in most statistical analyses, simplicity and ease of interpretation is important in research models. Thus, when there are uncertainties, which are inevitable in most anthropological analyses that are dependent on the population from which the estimates are derived, simplicity and replicability are equally important in developing models to investigate population relationships. Because of this, there is no useful purpose for arguing that cranial morphology is not a viable indicator of population relationships (Jantz and Owsley, 2003), and further research should be

undertaken on cranial heritability for as many populations and demographics as possible to get a more complete picture of the appropriateness of cranial traits in biodistance research.

Cranial Plasticity

From the last section, it is clear that skeletal traits have variable degrees of heritability, and, thus, it is important to consider other factors that can affect the phenotype of an individual. Such factors include epigenetic, developmental, climatic and functional causes. Epigenetic changes are also heritable but are caused by mechanisms, such as DNA methylation and histone deacetylation, other than changes in the underlying DNA sequence. In other words, epigenetic traits exist in addition to the traditional genetic basis of inheritance and can create different phenotypes in different cells (Bird, 2007; Russo et al., 1996). Epigenetics is a newer area of research and many aspects are not fully understood, so there has yet to be much consideration of these factors in craniometric biodistance analyses.

Franz Boas (1912) conducted research focusing on developmental and environmental plasticity. Between 1908 and 1910, Boas and his trained workers recorded a number of anthropometric measurements, including three cranial measurements, on thousands of European immigrants to the United States and two groups of offspring: European- and American-born. This data allowed a comparison of the effects of two environments during growth and development. Boas concluded, through laborious, non-computer assisted statistical methods, that the cranial measurements of the two groups of offspring were significantly

different, suggesting that siblings raised in different environments can have varying cranial measurements. Thus, environmental differences are capable of overriding heritability in Boas' estimation. This research was very influential in American anthropology, and there was a shift in the dominant ideology that cranial measurements reflect strictly genetics to the idea that the environment can play just as significant a role (Mielke et al., 2011).

Subsequent research in this area has found conflicting results. Two groups of researchers directly reanalyzed Boas's original data using the same statistical methods as well as newer, more sophisticated, methods (Gravlee et al., 2003; Sparks and Jantz, 2002). Even with using the same data, these groups reached different conclusions regarding the influence of plasticity on craniometrics. Gravlee and colleagues' (2003) emphasize results that were similar to those reported by Boas. In four out of the total seven immigrant groups studied, the researchers found a significant difference between the American-born and European-born immigrant offspring. Thus, these authors emphasize or exaggerate the immigration differences. Sparks and Jantz (2002) found different results. They reported only slight evidence for cranial plasticity, particularly in head shape. A recent publication by Jantz and Logan (2010) also provides an interpretation of Boas's findings.

Developmental plasticity is not the only aspect of the environment that can affect the phenotype of cranial traits. Climatic adaptation can also play a role. Research in this area may help illustrate short-term physiological adaptation and long-term natural selection and is particularly important to consider in research

focusing on the Late Pleistocene and Early Holocene eras, a time of considerable climate change.

There has been a great deal of research investigating the correlation of size and shape of the human head with climatic variation. Beals (1972) and Beals et al. (1984) concentrated on variation in cephalic index and general head measurements, and their results are in accordance with the Bergmann-Allen rules. Smaller and relatively narrow skulls lose more heat and are better adapted to hot climates; larger and relatively broader skulls retain heat and thus are better adapted for cold climates (Ruff, 1994).

Nasal size and shape has been an area of research in terms of climate correlation to head shape. There are claims of strong correlation between certain nasal measurements and ratios, particularly nasal index and temperature. Nasal index can be simply defined as the ratio of the width to the height of the nose. The measurement descriptions used to calculate the nasal index vary between researchers. Many in this area have found that populations native to colder climates have lower nasal indices, which reflects relatively high and narrow nasal openings. Native populations of hotter climates generally have higher nasal indices, which reflect relatively broad noses (Beals et al., 1984; Roberts, 1978). The nasal index is not only correlated to temperature but also humidity levels (Beall and Steegmann, 2000; Franciscus and Long, 1991). Even with the large amount of research indicating strong correlations between climatic factors and cranial traits, it is still uncertain how many generations or how extreme the climate must be to get an observable phenotypic change in a population.

Lastly, functional plasticity has also been suggested as an environmental factor that can dramatically shape craniofacial morphology. In particular, mechanical loads on the cranium and mandible have been studied in relation to masticatory forces (Gonzalez-Jose et al., 2005). Many have presented evidence that the reduction of masticatory muscles' activity, which can be caused by consuming soft foods produced from agriculture and heavily processed foods, is a main cause of reduction in muscle size associated with the skull, which has various consequences in bone (Beecher et al., 1983; Bresin et al., 1999; Carlson and Van Gerven, 1977; Giesen et al., 2003; Hannam and Wood, 1989; von Spronsen et al., 1991). However, some caution that if plastic responses to mechanical stressors are indicated in data, it is particularly important to estimate the magnitude of among-group variation in both overall craniofacial shape and localized structures (Gonzalez-Jose et al., 2005; Lieberman, 1997). Otherwise, misleading conclusions are possible. It is obvious from this synthesis on cranial heritability and plasticity that new research can bring more insight to biodistance analysis.

Traditional Metrics and Geometric Morphometrics

The use of geometric morphometrics (GM) has gained considerable attention in recent decades. Adams et al. (2004) claim that there was a "revolution" starting around the 1950s when researchers began to embrace the more sophisticated methods available through GM. Traditional morphometrics, i.e. point-to-point measurements, involve the collection of distances and angles through the use of standard tools, such as spreading and sliding calipers. These

measurements are one-dimensional. After collection, measurements are frequently subject to multivariate statistical procedures in order to answer questions concerning various anthropological questions. This type of morphometrics has been used for most of biological anthropology's existence and is still used successfully today. Many of the reburied remains of the first Americans were measured through traditional methods, and, therefore, this methodology will be of considerable importance here.

Recent arguments for the use of the more sophisticated techniques available through GM claim that traditional morphometrics fail to capture the complete spatial arrangement of the landmarks on which the measurements are based (Slice, 2007). The capturing of spatial arrangement is accomplished through GM. Most commonly through the use of digitizers, coordinates are collected either in two or three dimensions preserving important geometric relationships (Hennessy and Stringer, 2002; McKeown and Jantz, 2005). More sophisticated techniques are beneficial in capturing the subtle shape and size differences between different groups of people or individuals (Perez et al., 2005).

While multivariate statistical techniques can be used with traditional measurements, there is a very rigorous statistical theory developed specifically for GM shape analysis and often produce more accurate results than the traditional morphometric counterparts (McKeown and Jantz, 2005). Another benefit of GM analysis is the ability to take the coordinates and reproduce the shape of the original crania without actually returning to the original crania (Hennessy and Stringer, 2002). This is of particular importance in Paleoamerican

research where there is always the possibility that the skeletal material may be repatriated or reburied and further scientific research will no longer be possible. If three-dimensional coordinates are collected, this captures information that may be useful in further research if new analytical methods or questions become available.

The majority of GM methods utilized are landmark-based (Slice, 2007). These methods are similar to the traditional methodology in that both use biologically defined landmarks. However, the GM landmark-based methods are based on two- or three-dimensional (X, Y, Z) coordinates, which can later be used to calculate traditional measurements. Size variation should be removed from these methods, generally by some form of superimposition method, because the main goal of these types of methods is to better understand shape (Adams et al., 2004). Size is not a consideration here as is often the case with traditional methods. However, size is also patterned in space as well as time (Jantz and Ousley, 2005), and some disagree with the automatic removal of a potentially explanatory variable (Jungers et al., 1995).

Perhaps the most commonly used landmark-based GM method is Generalized Procrustes Analysis (GPA). This method compares forms by superimposing them according to a minimization criterion (Richtsmeier et al., 1992), often least squares estimates. After this step, shape differences can be described by the differences in coordinates of landmarks between objects, and this generally produces robust comparisons (Adams et al., 2004). There are several other methods that have produced promising results but are not as

commonly applied as GPA, such as thin plate splines, Euclidean distance matrices and finite scaling element analysis (Slice, 2007).

Although there are many benefits associated with GM, there are also several difficulties. The most important of these is assessing measurement error (von Cramon-Taubadel et al., 2007). Collecting traditional measurements is more conducive for observing incorrect measurements, particularly with experience. However, when all that is seen are coordinates, errors are easily concealed. In fact, an entire cranium can be digitized incorrectly, and this will not be realized until after completion, when assessing the measurements calculated from the coordinates. There are numerous ways to assess measurement error, such as specialized GPA and repeated digitization of landmarks while the specimen is in constant orientation, but these have problems of their own, such as the Pinocchio effect (van Cramon-Taubadel et al., 2007). Thus, there needs to be more effective means of assessing measurement error. Much of the data collected for this dissertation was obtained through geometric morphometric means. However, in order to compare to reburied remains and to compare the results found here with results in earlier research, the coordinates were converted into one-dimensional measurements.

Linking the Dead to the Living

The usage of biodistance analysis has increased as a result of laws on the repatriation or reburial of Native American remains in the United States. These types of analysis are used to better understand the biological and cultural links between living native groups and possible archaeological ancestors. This task is

made especially difficult due to geographic and temporal discrepancies as well as the fluidity of ethnic groups after contact (Larsen, 1997). Issues surrounding repatriation and reburial and biological anthropology will be discussed in Chapter Three as it plays a big role in the availability of data for this dissertation.

Chapter Three: Peopling of the New World

A different species? Who were the first Americans?

There have been recent discoveries and analysis of non-*Homo sapiens* specimens in far-reaching areas of the globe with dates contemporary to *Homo sapiens*, such as *Homo floresiensis* (Aiello, 2010). Thus, it is not unreasonable to discuss the possibility that the earliest Americans could be another species of the genus *Homo*. As generally accepted, the first early hominids to leave Africa were *Homo erectus* and its evolutionary kin (Anton, 2003; Meltzer, 2009). Their range seems to encompass most of Eurasia, and these individuals lived during glacial times, as would also the predecessors of the Paleoamericans, with a particular presence in Pleistocene Europe.

In addition, there is evidence that clothing may have been worn by these ancient peoples as revealed by associated remains of body lice (Kittler et al., 2003). As can be imagined, clothing would be imperative for survival in the very northern latitudes of Siberia and Beringia, if this is in fact the route by which the first migrants traveled. *H. erectus* and its descendants spread as far east as eastern Europe, China and southeast Asia, but there is yet to be any accepted evidence of these hominids in the far northeastern regions of Asia and certainly no evidence in the Americas (Anton, 2003; Meltzer, 2009). Thus, according to the current, available data, it appears that *Homo sapiens* were the first hominids to push to all regions of Asia and subsequently into the Americas.

What are the ancestral area(s) of the Paleoamericans?

There are numerous hypotheses regarding the ancestral area(s) of the earliest Americans. Evidence comes from a multitude of sources, such as morphometrics, dental anatomy, archaeology, geology, linguistics and genetics. This evidence will be discussed here by geographic area, and while craniometrics will be the means of exploration in this research, other sources of evidence will be considered in this section.

NORTHEAST ASIA

If the earliest Americans traveled by foot across Beringia into the New World, which is the traditional anthropological view, then the simplest explanation for the origin of these migrants would be from Northeast Asia. Archaeologically speaking, there has not been much evidence for early settlements of *Homo sapiens* in this area until rather late at least as far as the peopling of the New World is concerned. There is evidence that humans had reached Siberia before the last glacial maximum (LGM) with the sites of Nepa I in central Siberia dating to approximately 35,000 yr before present (BP) and Yana RHS in northern Siberia dating to 27,000 yr BP (Meltzer, 2009). However, both of these sites are still thousands of kilometers away from the eastern edge of Beringia (Meltzer, 2009). There is no archaeological evidence that northeastern Siberia was occupied at all during the LGM, possibly due to harsh climates during that time (Goebel, 2004; Hoffecker and Elias, 2003).

The more permanent settlement of this area did not occur until well after 18,000 yr BP, yet humans were still fairly scarce even then (Meltzer, 2009).

There are two securely dated sites in these northern latitudes but the dates are relatively late in terms of considering a possible role in the peopling of the New World: the site of Berelekh on the Indigirka river (14,000 yr BP) and Ushki in central Kamchatka (11,300 yr BP). These sites do contain distinctive Chindadn points, which are found with slightly later dates on the Alaskan side of Beringia (Meltzer, 2009). However, with these late dates for the few sites present, this presents a difficulty when considering sites in the Americas with comparable dates. It would be difficult for a northeast Asian wave of on-foot migrants to travel from the Siberian side of Beringia all the way to Chile in a couple of hundred years. If the earliest dates for Monte Verde are accepted (approximately 33,000 yr BP), this would make it virtually impossible. It is important to consider that these areas in Siberia have not had a strong archaeological presence, and perhaps if this changes, uncovering more sites can give a clearer picture of the occupation of this area.

Proponents of the Recurrent Gene Flow model, which will be discussed in more detail later in this chapter, argue that a highly, internally variable founding population, presumably from northeast Asia, was the likely source of the earliest Americans. After this initial expansion, there continued to be gene flow between northeast Asia and the Americas. This allowed for the dispersal of the commonly observed northeast Asian-derived characters found in modern Native Americans (de Azevedo et al., 2011).

Additionally, classic genetic research provides evidence for a northeast Asian ancestral area. Previous research on modern Native Americans reveals

that they fit within five mitochondrial DNA (mtDNA), A, B, C, D and X, and two Y-chromosome, C and Q, founding haplotypes. All of these genetic markers are found among indigenous populations of southern Siberia (Derenko et al., 2007; Goebel et al. 2008; Kemp and Schurr, 2010; Starikovskaya et al., 2005; Zegura et al., 2004). Thus, there appears to be strong evidence that northeast Asia was the ancestral area for modern Native Americans but not necessarily Paleoamericans.

GENERALIZED EAST ASIA

The majority of dental evidence points towards an eastern Asian origin for the earliest Americans. Certain traits, specifically maxillary central and lateral incisor shoveling, have been noted in high frequencies in both Native American and eastern Asian populations (Carbonell, 1963; Dahlberg, 1968; Hanihara, 1992; Hrdlicka, 1920; Turner, 1969, 1983, 1990). This suite of traits is often referred to as the ‘”Mongoloid dental complex” (Hanihara, 1968) or Sinodonty (Turner, 1983, 1990) and involves not only shoveling but high frequencies of mandibular first molar deflecting wrinkle, protostylid, entoconulid and metaconulid (Hanihara, 1968). Additionally, there is growing support from genetic research for eastern Asia as the ancestral area of the earliest Americans as well as modern Native Americans (Bonatto and Salzano, 1997a, b; Merriweather et al., 1995; Santos et al., 1999; Silva et al., 2002).

Archaeologically, there has been little extensive analysis directly comparing the technological styles of ancient East Asians and that of the earliest Americans or even Clovis people. Most studies focus specifically on comparing

the American toolkit to northeast Asian ones. However, there is a strong archaeological presence in East Asia, unlike in northeast Asia, and hopefully there will be more direct comparisons soon. While there is some craniometric evidence indicating a generalized East Asian origin (Brace et al., 2004; Sardi et al., 2005), some researchers argue that there is no morphological affinity between the earliest Americans and eastern Asians (Neves et al., 2004, 2007).

SOUTHEAST ASIA AND/OR PACIFIC RIM POPULATIONS

The best evidence for southern Asia and/or the Pacific Rim as the ancestral areas for the earliest Americans comes from morphological data, specifically craniometrics. Several researchers have provided results indicating that many early American individuals or groups have phenotypic associations with populations from this area (Jantz and Owsley, 2005; Neves et al., 2007; Steele and Powell, 2002). The associations are generally shown through biodistance statistical analysis of craniometric data (Jantz and Owsley, 2005; Neves et al., 2007), but some authors simply describe traits that these populations share (Steele and Powell, 2002). There has been little support from other research areas but this could be attributed to lack of investigation.

EUROPE

Most of the support for a European ancestral area for the earliest Americans comes from the first interpretations of the Kennewick individual's cranial morphology by James C. Chatters, who reported the biological heritage of the individual as 'Caucasoid;' however, there was confusion surrounding the

initial discovery. This caused a media frenzy with articles written in *The New Yorker* and *US News and World Report,* among others, all alluding to the idea that Europeans may have colonized the Americas before Asians (Thomas, 2000). A facial reproduction was also produced which many have suggested to favor the Caucasian actor, Patrick Stewart (Powell, 1999).

There has been substantial re-analysis of the Kennewick cranium, including by James Chatters (Chatters, 2001), most find that there are more significant similarities with East Asian populations (Brace et al., 2002; Powell, 2005; Powell and Neves, 1999). Additionally, there is a subset of archaeologists who believe migrants using the European, Solutrean culture were among the first settlers of the New World (Stanford and Bradley, 1999, 2002, 2012). However, many archaeologists refute these claims (Strauss, 2000).

Migration Scenarios into the Americas

The question of how many migrations from the Old World into the New World it took to obtain the diversity that is seen between Paleoamericans, Archaic and modern Native Americans has intrigued anthropologists for decades, particularly those specializing in morphometrics, linguistics, genetics and archaeology. This section will introduce the three main theories and a newer, intriguing hypothesis regarding migration scenarios for the peopling of the New World.

OUT OF BERINGIA (SINGLE WAVE) MODEL

The Single Wave model gains most of its support from conclusions established by genetic research. With the influx of analysis in this area over the past 20 years, there are two recurrent conclusions. First, for certain lineages of Y-chromosome, mtDNA and autosomal genomes of Native Americans, there is an accumulation of mutations (Fagundes et al., 2008a, b; Tamm et al., 2007). Using the pattern and number of these mutations, several researchers were able to compute approximate dates of isolation, in addition to the duration and magnitude of expansions or bottlenecks that these founding populations experienced (Bonatto and Salzano, 1997a; Fagundes et al., 2008 a, b; Tamm et al., 2007). With this information, the most parsimonious explanation would be a single ancestor group traveling from northeastern Asia, in one wave, that was confined in Beringia (often referred to as the Beringian standstill) during the Late Pleistocene. The second recurrent conclusion is that there is a molecular coalescence of most modern Native Americans to a unique ancestral population somewhere in eastern Asia (Bonatto and Salzano, 1997a, b; Merriweather et al., 1995; Santos et al., 1999; Silva et al., 2002), further arguing for one wave into the Americas.

Although the majority of morphometric analysis proposes more than one migratory event, there are some that explain the major morphometric diversity as a result of *in-situ* evolution. Powell and Neves (1999) argue that the diversity may be the result of a single migratory event in which the Paleoamerican or founder population underwent great change in the Americas by means of genetic drift.

TWO COMPONENTS (TWO-WAVES) MODEL

The Two Components model is based on findings indicating the presence of two differentiated craniofacial morphologies in the Americas. This is interpreted as the result of two distinct source populations from Asia coming to the New World at different times (Hubbe et al., 2010; Neves and Hubbe, 2005; Neves and Pucciarelli, 1991; Pucciarelli et al., 2003). This model is useful in explaining the differentiation between the craniometrics of early Americans and modern Native Americans found by researchers, such as Neves and Pucciarelli (1991) and Pucciarelli et al. (2003). Thus, there are two distinct morphologies resulting from two waves of migration in this model. The first are the Paleoamericans, which represent the first wave originating possibly from southeastern Asia. The second category consists of “Amerindians,” representing the second wave from eastern Asia during the early Holocene. The second wave virtually replaced the Paleoamericans, and this explains why researchers do not see the “typical” Paleoamerican craniofacial morphology in modern Native Americans.

There has been a growing amount of re-analysis of this hypothesis. Perez and coworkers (2009) included both craniometric as well as ancient DNA (aDNA) data from central Argentina. Like many other studies, the craniometric data supports the Two Components theory; however, the aDNA showed that all individuals studied shared the same mtDNA haplotype. This discontinuity between craniometric and genetic data is not an uncommon occurrence in peopling of the New World research, and there are several possible explanations

for it, such as drift, selection and plasticity (Perez et al., 2009; Raff et al., 2011). Additionally, there is evidence that the craniofacial morphology common in Paleoamericans can also be found in pockets of modern Native American groups (Gonzalez-Jose et al., 2003; Pucciarelli et al., 2008; Vezzani Atui, 2005). A last note is that many of the studies supporting the Two Components model are heavily skewed with regards to the data utilized, as most focus on South American individuals or samples.

TRIPARTATE (THREE-WAVES) MODEL

The Tripartite model, proposed by Greenberg et al. (1986), is lauded for being one of the first studies attempting to incorporate interdisciplinary lines of evidence (linguistics, dental anthropology and genetics) to answer questions surrounding migrations into the Americas. However, there has been very little support for this model from other researchers (Crawford, 1998; Gonzalez-Jose et al., 2003; Merriweather et al., 1995; Powell, 1995; Pucciarelli et al., 2003; Stone and Stoneking, 1998; Szathmary, 1986, 1994).

In this model, three temporally-separate migrations occurred in the New World and gave rise to three main linguistic groups found in the Americas: Amerindian, Na-Dene and Aleut-Eskimo. All of these migrations originated in eastern Asia. The first migration was comprised of Paleoindians and gave rise to present day Amerind-speaking Native American populations that occupy a large geographic area: South, Central and most of North America. The second wave involved Na-Dene speakers, such as the Navajo and Athabaskan, which occupied the interior of Alaska and some southwest portions of the United

States. Lastly, the third, independent migration was the Eskimo-Aleut who presently inhabit the Arctic and sub-Arctic lands (Greenberg et al., 1986). All three forms of evidence presented by Greenberg et al. (1986) have been heavily criticized (Crawford, 1998; Merriweather et al., 1995; Powell, 1995), and more recent and sophisticated analyses have yet to provide further support for the Three Waves model.

RECURRENT GENE FLOW MODEL

While the Single Wave model seems to be the best explanation for the genetic evidence and the Two Waves model has support from morphological data, both models fail to provide an integrative view of more than one type of evidence. The Three Waves model provides a unified view among disciplines but does not have much support from additional and more sophisticated research. The shortcomings of all these models brought about the development of the Recurrent Gene Flow model (de Azevedo et al., 2011). This theory was built on both recent molecular research and reinterpretations of craniofacial variation presented in Gonzalez-Jose et al. (2008). This model characterizes the ancestral population for the earliest Americans as internally diverse both craniofacially and genetically. This founding population occupied Beringia during the last glaciation and then expanded throughout the New World. After and possibly during this expansion, there was additional Circum-Arctic gene flow, which enabled the dispersal of northeast Asian characteristics into the Americas (de Azevedo et al., 2011).

In regards to the molecular evidence, these authors specifically cite newer research supporting a possible early gene flow with the Arctic representatives of American and Asian populations well before the formation of the Bering Strait, presented by Gilbert et al. (2008), Mulligan et al., (2008), Rasmussen et al. (2010), Tamm et al. (2007), Volodko et al. (2008) and Zlojutro et al. (2006). In terms of the craniometric analysis, the authors argue that when avoiding *a priori* labels such as Paleoamerican/Indian, Amerindians and Mongoloids, results indicate that the variation is not separated into discrete units but rather represents a much more fluid and continuous sample (de Azevedo et al., 2011). Thus, through their analysis of 2D geometric morphometric data and design matrices, de Azevedo et al. (2011) support the Recurrent Gene Flow model. This model is also appealing because it has aspects of both the Single Wave and Two Component models. However, since this is a new model, there is little additional support and some portions of this theory are yet to be fleshed out.

Chapter Four: Materials

This chapter describes and categorizes the various samples or individuals that are used in this dissertation. Geographic locations, sample sizes, sex, dates and references are presented. The latitudes and longitudes of the skeletal material sites are given, which are used to construct spatial and design matrices. Lastly, the craniometric dimensions utilized in this analysis are also provided.

Paleoamerican sample

As the focus of this dissertation is to obtain a better understanding of the migration routes and ancestral areas of the Paleoamericans, more detail is presented concerning the Paleoamerican sample. Most sites discussed have only one associated individual, but there are a few that have slightly larger sample sizes. An individual is considered part of the larger Paleoamerican sample if there are published dates of 8000 yr BP or earlier associated with the skeletal material. North, Central and South American Paleoamericans are described in this section. Table 1 provides a synopsis of this information.

ARCH LAKE SITE, NEW MEXICO

The Arch Lake site was discovered in 1967 in New Mexico and contained an adult female. The remains are housed at the Blackwater Draw Museum at Eastern New Mexico University. The Arch Lake remains date to 10,020 yr BP based on recent radiocarbon dating. An interdisciplinary team led by Douglas Owsley of the Smithsonian Institution reevaluated the burial material in February 2000 (Owsley et al., 2010).

Table 1: Paleoamerican sample details

Specimen	Region/Location	Sex	Mean Age	Reference
Arch Lake	North America/ New Mexico	F	10020[1]	Owsley et al., 2010
Browns Valley	North America/ Minnesota	M	8800[1]	Myster and O'Connell, 1997
Buhl	North America/ Idaho	F	10625[1]	Taylor, 1994
Cerca Grande 6 & 7	South America/ Brazil	2M; 3F	9325[1]	Hunt, 1960; Gonzalez-Jose et al., 2005
Chimalhuacan	Central America/ Mexico	M	10500[1]	Gonzalez et al. 2002
C. del Tecolote	Central America/ Mexico	M	8000[2]	Pompa y Padilla and Serrano Carreto, 2001
Gordon Creek	North America/ Colorado	F	9400[1]	Swedlund and Anderson, 1999
Kennewick	North America/ Washington	M	9400[1]	Chatters, 2000
Lapa Vermelha IV	South America/ Brazil	F	9330[3]	Gonzalez-Jose et al., 2005
Lime Creek Burial	North America/ Nebraska	M	9524[1]	Key, 1983
Metro Balderas	Central America/ Mexico	M	10500[2]	Arce et al., 2003
Penon III	Central America/ Mexico	F	10755[4]	Gonzalez-Jose et al., 2005
Spirit Cave	North America/ Nevada	M	9430[5]	Powell, 2005
Sumidouro	South America/ Brazil	9 M; 4 F	8000[6]	Neves et al., 2007
Toothpick	North America/ Washington	M	9000[1]	Chatters, 2001
Tlapacoya	Central America/ Mexico	M	10200[1]	Lorenzo and Mirambell, 1986
West Gravel Pit	North America/ Nebraska	1 M; 1 F	9500[2]	Key, 1983
Wizards Beach	North America/ Nevada	M	9225[1]	Dansie, 1997

[1] Carbon-14 age; [2] Stratigraphic/ geological age; [3] Minimum AMS age; [4] Exact AMS age; [5] Total amino acids; [6] Carbon-14 on other organic materials

BROWNS VALLEY SITE, MINNESOTA

The Browns Valley individual is a robust male found in association with Terminal Pleistocene Yuha and Folsom-like points (Powell, 2005). The Browns Valley skeleton was discovered on October 9, 1933 by amateur archaeologist, William H. Jensen, and Albert Jenks investigated this site in 1933 and 1934 (Jenks, 1936, 1937). Although originally thought to be much older and was compared to *Homo heidelbergensis* in terms of robusticity, this skeleton yields ^{14}C ages of 8700 ± 110 yr BP and 8900 ± 80 yr BP through accelerator mass spectrometry (AMS) (Myster and O'Connell, 1997). The skeletal and cultural remains were reburied on October 2, 1999 in South Dakota by the Sioux tribes (Friends of the American Past).

BUHL SITE, IDAHO

The Buhl skeleton was discovered by non-archaeological construction at a rock quarry in Buhl, Idaho. The human remains are those of a young female, estimated to be around the age of 17 to 21 at death with various pathologies, such as dental attrition and Harris lines (Green et al., 1998). Under the skull, an unused obsidian biface was found in addition to the eyelet of a bone needle. The fact that these artifacts were found directly under the skull suggests that the body may have been intentionally buried (Green et al., 1998). A radiocarbon age of 10,625 ± yr BP (BETA-430055/ETH-7729) was obtained from a piece of bone using total acid-insoluble organics (Taylor, 1994). The Buhl skeletal material was reburied in 1991 by the Shoshone Bannock tribe (Friends of the American Past).

CERCA GRANDE SIX AND SEVEN, LAGOA SANTA SITES, BRAZIL

Cerca Grande 6 and 7 are large rock shelters associated with the terminal Pleistocene and early Holocene eras. They were discovered by Johannes Lund and excavated by Wesley Hurt (1960). There are associated rock shelters (1-5) dating to the Late Archaic, and these have more skeletal remains. The rock shelters of Cerca Grande 6 and 7 contained 10 mostly complete skeletons and many others with heavily fragmentary remains. Cerca Grande 6 had four fragmentary crania while Cerca Grande 7 had one complete cranium. Most of the materials from Cerca Grande are currently housed at the Museu Nacional do Rio de Janiero (National Museum in Rio de Janeiro). The rest of the skeletal material and some of the associated megafauna are located in various museums in Europe. Radiocarbon dates were obtained from human bone collagen samples. Shelter 6 materials ranged between 9,028 and 9,720 yr BP with a median age of 9,374 yr BP, and the Shelter 7 individual's median age was 9,130 yr BP (Hunt, 1960; Powell and Neves, 1999).

CHIMALHUACAN SITE, MEXICO

The Chimalhuacan Man is a mostly complete skeleton discovered in 1984 in Colonia Embarcadero (Chimalhuacan, Estado de Mexico). There are many problems in terms of dating the skeletal material. Like many ancient Mexican skeletons, there is strong mineralization, and thus, no collagen preservation in the skeleton. Additionally, there are no published records of stratigraphy for this site. Therefore, indirect dating is the only means of establishing age for this skeletal material. Sediments found inside the skull, which consist of a mixture of

lake sediments, diatoms and volcanic ash from the Upper Toluca Pumice, produced dates at around 10,500 radiocarbon years before present (RCYBP) (Gonzalez et al., 2002). This skeleton was found in association with obsidian flakes and some bone tools (Gonzalez-Jose et al., 2005).

CUEVA DEL TECOLOTE SITE, MEXICO

In 1959, Cynthia Irwin Williams discovered two cave burials in Huapalcalco (Estado de Hidalgo). Only one of these burials had substantial cranial remains, and this is what is analyzed here. Unfortunately, similar to the Chimalhuacan specimen, there is no collagen preservation in the skeletal material. Based on stratigraphy and archaeological affinities, the Tecolote skull was dated to 9000-7000 years before present (Pompa y Padilla and Serrano Carreto, 2001). These burials were discovered with offerings, a canid mandible and five complete dogs (Gonzalez-Jose et al., 2005; Romano, 1974).

GORDON CREEK SITE, COLORADO

The Gordon Creek Woman was discovered in a burial pit lying on her left side in a flexed position with head pointing north. The burial was found in association with a hammerstone, flakes, a smooth grinding stone and two bifaces (Breternitz et al., 1971). This skeleton was initially determined to be a male (Breternitz et al., 1971); however, a more detailed analysis of the material by a group of anthropologists determined that this skeleton represents a female (Swedlund and Anderson, 1999). A ^{14}C date of 9400 ± 120 yr BP places this individual in the Paleoamerican category (Swedlund and Anderson, 1999).

KENNEWICK SITE, WASHINGTON

Although mostly complete, the Kennewick Man's remains are damaged, but this skeleton provides important clues into Paleoamerican life ways. Kennewick Man was a 40 to 45 year old male with a fracture on the left side of the skull and evidence of arthritis and severe dental disease. Evidence of trauma on the Kennewick skeleton includes the Cascade projectile point found embedded in the right iliac blade (Chatters, 2000; Powell and Rose, 1999). This was the first clue that this individual was of interest in the Paleoamerican discussion.

With this strong evidence of the skeleton's antiquity, further testing was completed and a radiocarbon test dated the Kennewick skeleton to between 9200 and 9600 RCYBP, with an average ^{14}C age of 9400 yr BP (Chatters, 2000; Chatters et al., 1999). Refer to Chapter One for a more detailed description of the Kennewick skeleton and the role the NAGPRA plays in its availability for scientific study.

LAPA VERMELHA IV, LAGOA SANTA SITES, BRAZIL

The Lapa Vermelha site is a rockshelter that is part of a larger karst complex of caves, shelters and underground rivers (Laming-Emperarie et al., 1975). It is located in the state of Minas Gerais in central Brazil. This site has a thick layer of both Pleistocene and early Holocene deposits that date as far back as 22,410 yr BP with evidence of human occupation dating to 11,000 yr BP (Dillehay et al., 1992; Prous, 1980, 1986, 1991; Schmitz, 1984, 1987) and well-

preserved bones of a giant sloth (*Glossoterim gigus*) dating to 9580 ± 200 yr BP (Laming-Emperaire, 1979).

About 2 meters below the giant sloth, the unarticulated remains of a human skeleton were found. These remains were found bracketed between two archaeological levels with radiocarbon dates of 11,600 yr BP and 12, 960 yr BP (Prous, 1986). There have been some questions regarding the stratigraphic positioning (Cunha and Mello e Alvim, 1971), but an AMS date on total organics of the sample produced a minimum age of 9330 ± 60 yr BP (BETA-84439). The skeletal remains, nicknamed “Luzia,”, are those of an adult female aged 20 to 25 years at death. These are not the only skeletal remains found at this site but they are the oldest and thus receive the majority of attention in discussions of Paleoamericans.

LIME CREEK BURIAL SITE, NEBRASKA

Several skeletons were found during the excavation of the Lime Creek site between 1947 and 1950 in southern Nebraska. It is believed that these Paleoamerican people camped on the banks of the Lime Creek channel, protected from the cold, northerly winds by a large bluff (Conyers, 2000). The skeletons are in variable levels of preservation, and only one male cranium will be included in this analysis, as it is the most complete. All skeletal materials have been repatriated and reburied with little anthropological analysis. There are some questions surrounding the possible stratigraphic association of this material and terminal Pleistocene deposits (Powell, 2005), but ^{14}C dates of 9974-9074 yr BP, with a median age of 9524 yr BP, have been published (Key, 1983).

METRO BALDERAS SITE, MEXICO

The Metro Balderas skull is a male dating to approximately 10,500 RCYBP (Arce et al., 2003). The skull was discovered in 1970 during construction work at the Balderas Metro station in Mexico City (Gonzalez-Jose et al., 2005). Due to the lack of collagen preservation, no radiocarbon testing was possible. However, two separate means of dating suggest an early date. Stratigraphically, the skull was embedded in one of the main tephra markers for the Basin of Mexico (the Tripartite Ash or Upper Toluca Pumice), which has been reevaluated and dated to 10,500 RCYBP (Arce et al., 2003). Additionally, volcanic ash samples found within the skull were analyzed using microprobe analysis and give values associated with the Upper Toluca Pumice eruption (Gonzalez et al., 2001).

PENON SITE, MEXICO

The Penon partial skeleton, often referred to as Penon Woman III, was originally discovered at the Mexico City airport in 1959 but sat in the Mexico City's National Museum of Anthropology until 2001. Specifically, the skeleton was found around the Penon de los Banos Hill, which during the Late Pleistocene was an island surrounded by hot springs in the middle of Texcoco Lake (Gonzalez-Jose et al., 2005; Mooser and Gonzalez Rul, 1961). Due to reported radiocarbon dates of older 13,000 yr BP, interest in this skeleton reemerged (Powell, 2005). Unlike most ancient Mexican skeletal material, direct testing was possible on actual bone, the humerus, which was directly dated by accelerator mass spectrometry to 10,755 ± 75 RCYBP (Gonzalez-Jose et al., 2005).

SPIRIT CAVE SITE, NEVADA

The Spirit Cave skeleton (AHUR-743), often referred to as Spirit Cave Man, is a well preserved human mummy, including hair, that was found in association with a wide range of cultural material, such as a rabbit-skin blanket, leather moccasins and a sage-filled burial mat. In addition to the mummy, there were two cremations discovered at the site. The male skeleton has been estimated to be 35-40 years old at death with a high level of pathology, such as extreme attrition, multiple abscessed teeth, periodontal disease, a partly healed pre-mortem fracture of the right wrist, small fracture on the left side of the skull and arthritic degeneration (Powell, 2005).

From the mummified body's bone collagen, total amino acids revealed a date of 9,430 ± 60 yr BP (URC-3260/CAMS-12352) (Powell, 2005). Due to the overlying soft tissue on the crania, an epoxy resin cast was produced by the Nevada State Museum. It is from this cast that cranial measurements are taken.

The Spirit Cave skeleton has had several NAGPRA claims based on proximity to tribal traditional lands. The United States Bureau of Land Management, determined, that based on current evidence and analysis, they could not assign the Spirit Cave skeletal material to any tribe (Barker et al., 2000). Therefore, the remains are currently in federal possession.

SUMIDOURO, LAGOA SANTA SITES, BRAZIL

The Sumidouro Cave is one of the hundreds of caves recorded in the Lagoa Santa karst, located approximately 30 kilometers from the state capital of Minas Gerais. The Danish naturalist, Peter W. Lund, was the first to explore these caves and created a large human skeletal and megafaunal collection, referred to as the Lund collection (Lund, 1844; Plio and Auler, 2002).

There were approximately 30 early Holocene specimens recovered from the Sumidouro Cave. However, due to fragmentation and lack of cranial material in many of these specimens, only nine males and four females will be included in this analysis. Even with this reduction, this assemblage is the largest collection of early American skulls from a single site or environment (Neves et al., 2007).

No collagen was preserved in any of the skeletal material, which may be due to oscillation of the water table within the chambers. Thus, no absolute dates can be generated for these remains. A shell inserted into a human auditory meatus was dated to a calibrated interval of 8530-8200 BP, while a sample of charcoal adhering to a human postcranial bone was dated to a calibrated interval of 8540-8390 BP. Other materials have produced dates similar to those described (Neves et al., 2007). These dates are congruent with the opinion that the peak of human occupation in Lagoa Santa occurred between 9500 and 7500 years BP, with most of the organized cemeteries being established in local rock shelters through Lagoa Santa from 8500 to 7500 BP (Araujo et al., 2005).

The Lund collection containing the Sumidouro material is found at the Zoology Museum of the University of Kopenhagen, the Museum of Natural History, London and the Historic and Geographic Institute, Rio de Janerio.

TOOTHPICK/STICKMAN SITE, WASHINGTON

The Toothpick partial skull was re-discovered by James Chatters on a museum shelf at Central Washington University. Chatters noted similar features of this skull and the Kennewick skull. Re-analysis of the dates associated with this skeletal material produced an age of approximately 9000 yr BP. The skull was found in northeastern Quincy Basin just east of the Colombia River in central Washington about 100 miles northeast of the Kennewick site (Chatters, 2001).

TLAPACOYA I SITE, MEXICO

The Tlapacoya skeletal material was discovered on Tlapacoya Hill in the southeast portion of the Basin of Mexico in the former Chalco Lake. Motorway workers uncovered this skull in 1962, and therefore, stratigraphy was not recorded (Gonzalez-Jose et al., 2005). Fortunately, direct dating of the cranium was possible by accelerator mass spectrometry, which produced a date of 10,200 ± 65 RCYBP (Lorenzo and Mirambell, 1986).

WEST GRAVEL PIT SITE, NEBRASKA

A male and a female skeleton were uncovered at the West Gravel Pit site in Nebraska. There have been questions regarding the stratigraphic association with terminal Pleistocene deposits (Powell, 2005). Key (1983) published dates of

10550 to 8550 with a median age of 9550 through geological analysis. The skeletal remains have been repatriated and reburied with little scientific analysis.

WIZARDS BEACH SITE, NEVADA

The Wizards Beach skull was discovered in 1978 on an ancient beach, Pyramid Lake in Washoe County, after it was exposed by low water in the Pyramid Lake Indian Reservation. The skull was only partially buried and therefore had differential staining of the skull. The skeleton is an adult male with poor dental health (Steele and Powell, 1999). There is the possibility of repatriation to the Paiute tribes from the Pyramid Lake Paiute Indian Reservation, but as of now, the remains have not been reburied (Friends of the American Past). This skeleton has been dated to 9225 RCYBP (Dansie, 1997; Tuohy and Dansie, 1996, 1997).

Archaic Individuals and Samples

The Archaic sample consists of 106 individuals from North and South America dating between 7999 to 1000 yr BP. This sample will serve as a comparison to the Paleoamerican sample as well as a vital part of the re-analysis of previously proposed hypotheses regarding migration scenarios and ancestral areas. There are a few of these individuals or samples that have a published date of earlier than 8000 yr BP, such as Tequendama, Sauk Valley and Windover; however, there are a larger quantity of published dates after 8000 yrs BP. Thus, they will be placed in the Archaic category. Refer to Table 2 for pertinent information regarding the Archaic sample.

Modern, Worldwide Comparative Data

Comparative data include late Holocene and modern populations and were obtained from large worldwide samples of human crania analyzed by W.W. Howells (1973, 1986, 1989). This data set was chosen for three reasons: ease of retrieval, prolific use in similar studies (Azevedo et al., 2011; Gonzalez-Jose et al., 2001, 2005; Hubbe et al., 2010; Jantz and Owsley, 1998; Munford et al., 1996; Neves and Pucciarelli, 1989; Neves et al., 1997, 1999; Powell and Neves, 1999) and most importantly, the variables and variable descriptions used by Howell are the same as used in this dissertation. Detailed information about the variables is available in Howells (1973, 1989), and original data was downloaded from the website http://konig.la.utk.edu/howells.htm. These data represent regional phenotypic variation prior to the extensive migration and population growth of the last 500 years (Powell and Neves, 1999). Refer to Table 3 for pertinent information regarding the worldwide data set.

Latitude and Longitude

In order to construct the spatial matrices that are used as a comparison to the biological distance matrix, latitudes and longitudes are needed. While there is ample sample size for each of the worldwide, comparative populations, many of the individuals in the Paleoamerican and Archaic categories had to be pooled in order to have adequate sample size. The groupings are as follows: North American Paleoamericans, Central American Paleoamericans, South American Paleoamericans, Midwestern North American Archaics, Southeast North

Table 2: Archaic sample details

Specimen	Region/ Location	Sex	Mean Age	References
Aguazuque	South America/ Columbia	9 M; 10 F	5030[1]	Correal, 1990
Bahm Burial	North America/ North Dakota	2 M; 3 F	Archaic[3]	Key, 1983
Checua	South America/ Columbia	1 M; 2 F	7300[1]	Groot, 1992
Chia	South America/ Columbia	2 F	5040[1]	Ardila, 1984
Dry Lake	North America/ Nebraska	3 F	1250[2]	Key, 1983
Fish Hatchery	North America/ Nebraska	F	Archaic[3]	Key, 1983
Gilder Mound	North America/ Nebraska	F	Archaic[3]	Powell, 2005
Grant County Burial	North America/ North Dakota	M	Archaic[3]	Key, 1983
Lagoa Santa	South America/ Brazil	11 M; 7 F	7500[1]	Neves and Hubbe, 2005
Medicine Crow	North America/ South Dakota	M	3500[2]	Key, 1983
Pelican Rapids	North America/ Minnesota	F	7840[1]	Myster and O'Connell, 1997
Plattsmouth Ossuary	North America/ Nebraska	1M; 1 F	3175[2]	Powell, 2005
Sauk Valley	North America/ Minnesota	M	4275[1]	Powell, 2005
Swanson Lake	North America/ Nebraska	M	4500[3]	Jantz and Owsley, 2001
Tequendama	South America/ Colombia	5 M; 4 F	7500[1]	Correal and van der Hammen, 1977
Trego County Burial	North America/ Kansas	M	Archaic[3]	Key, 1983
Turin	North America/ Iowa	M	4720[3]	Jantz and Owsley, 2001;Fischer et al., 1985
Windover	North America/ Florida	15M; 19 F	7777[1]	Doran and Dickel, 1988
Young Burial	North America/ Kansas	2F	3200[3]	Witty, 1982

[1] Carbon-14 age; [2] Stratigraphic/ geological age; [3] Unknown

Table 3: Worldwide sample details

Group Name	Region/ Location	Sample Size
Ainu	East Asia/ Japan	48 M; 38 F
Andaman Islands	Southeast Asia/ Andaman Islands	35 M; 35 F
Anyang	East Asia/ China	42 M
Arikara	North America/ Kansas	42 M; 27 F
Atayal	Southeast Asia/ Taiwan	28 M; 17 F
Australia	Australia/ South Australia	52 M; 49 F
Berg	Europe/ Austria	56 M; 53 F
Buriat	Northeast Asia/ Siberia	55 M; 54 F
Bushman	Africa/ South Africa	41 M; 49 M
Dogon	Africa/ Mali	47 M; 52 F
Easter Island	Polynesia/ Easter Island	49 M; 37 F
Eskimo	Northern North America/ Greenland	53 M; 55 F
Guam	Micronesia/ Guam	30 M; 27 F
Hainan	East Asia/ China	45 M; 38 F
Maori	Polynesia/ New Zealand	21 M
Mokapu	Polynesia/ Hawaii	51 M; 49 F
Moriori	Polynesia/ Chatham Islands	57 M; 51 F
Norse	Europe/ Norway	55 M; 55 F
North Japan	East Asia/ Japan	55 M; 32 F
Peru	South America/ Peru	54 M; 54 F
Philippines	Southeast Asia/ Philippines	50 M
Santa Cruz	North America/ California	51 M; 51 F
South Japan	East Asia/ Japan	50 M; 41 F
Tasmania	Australia/ Tasmania	45 M; 42 F
Teita	Africa/ Kenya	33 M; 50 F
Tolai	Melanesia/ New Britain	56 M; 54 F
Zalavar	Europe/ Hungary	53 M; 45 F
Zulu	Africa/ South Africa	55 M; 46 F

American Archaics, Colombian Archaics and Brazilian Archaics. Average latitudes and longitudes were computed for these groupings, which are composed of a multitude of sites. Refer to Table 4 for a list of associated latitudes and longitudes.

Craniometric Dimensions

For many of the individuals and samples listed in Tables 1, 2 and 3, up to 60 craniometric dimensions were recorded. However, differential preservation of the remains and the lack of univariate normality for some variables limited the analysis to the 17 craniometric dimensions listed in Table 5. The data was collected by both geometric morphometric and traditional means. Descriptions of the measurements can be found in Howells (1973, 1989). This author collected a large portion of the data, while significant numbers were also collected and compiled by Richard Jantz and Walter Neves and generously given to this author for use in this dissertation. Additionally, as described above, the worldwide, comparative data set was collected and compiled by Howells (1989). Other data was obtained from published sources (Gonzalez-Jose et al., 2005; Neves et al., 2007) and Walter Neves collected the data within these publications. Refer to Table 5 for the dimensions utilized in this dissertation.

Table 4: Latitudes and longitudes for populations and groupings

Population	Latitude	Longitude
Ainu	43.23°	142.70°
Andaman Islands	11.74°	92.65°
Anyang	36.10°	114.39°
Arikara	44.45°	-100.40°
Atayal	25.05°	121.61°
Australia	-35.16°	147.38°
Berg	46.72°	14.18°
Brazilian Archaic	-19.63°	-43.89°
Buriat	51.68°	103.70°
Bushman	-28.45°	26.81°
Central American Paleoamerican	21.05°	-101.94°
Colombian Archaic	4.57°	-73.97°
Dogon	14.54°	-3.66°
Easter Island	-27.12°	-109.37°
Eskimo	60.90°	-48.35°
Guam	13.51°	144.80°
Hainan	20.03°	110.34°
Maori	-40.87	175.01°
Midwest North American Archaic	42.70°	-98.46°
Mokapu	21.44°	-157.75°
Moriori	-44.01°	-176.54°
Norse	59.91°	10.74°
North American Paleoamerican	39.99°	-107.78°
North Japan	43.06°	141.35°
Peru	-12.46°	-75.92°
Philippines	14.59°	120.98°
Santa Cruz	34.01°	-119.78°
South American Paleoamerican	-21.53°	-43.25°
Southeast North American Archaic	27.65°	-81.51°
South Japan	33.00°	131.00°
Tasmania	-41.72°	146.17°
Teita	-3.40°	38.55°
Tolai	-5.75°	150.77°
Zalavar	46.67°	17.16°
Zulu	-26.46°	27.77°

Table 5: Craniometric dimensions

Measurement/ Abbreviation	Measurement/ Abbreviation
Glabello-occipital length/ GOL	Nasio-frontal subtense/ NAS
Nasio-occipital length/ NOL	Cheek height/ WMH
Maximum cranial breadth/ XCB	Nasion-bregma chord (Frontal chord)/ FRC
Maximum frontal breadth/ XFB	Nasion-bregma subtense/ FRS
Biauricular breadth/ AUB	Nasion-bregma fraction/ FRF
Biasterionic breadth/ ASB	Bregma-lambda chord (Parietal chord)/ PAC
Orbital height/ OBH	Bregma-lambda subtense/ PAS
Interorbital breadth/ DKB	Bregma-subtense fraction/ PAF
Bifrontal breadth/ FMB	

Chapter Five: Methods

This chapter describes the methodology utilized to address the questions surrounding the ancestral areas and migration routes of the earliest Americans.

Missing Data

The reduced variable set shown in Table 5 maximizes the completeness of the Paleoamerican and Archaic data matrices but did not eliminate the problem of missing values altogether. In order to complete most statistical analyses for this research, missing values had to be estimated. This was completed through an expectation-maximization (EM) algorithm through the computer program SAS. This is a technique that finds maximum likelihood estimates in parametric models for incomplete data (McLachlan and Krishnan, 1997; Schafer, 1997). This algorithm is an iterative procedure with two steps. The first, expectation, step calculates the conditional expectation of the complete-data log likelihood given the observed data and parameter estimates. The second, maximization, step finds the parameter estimates that maximize the complete-data log likelihood from the previous step. These two steps are iterated until the iterations converge. Out of the 595 data points for the Paleoamerican sample, 46 were estimated by this method (around 8%). Out of the 1887 data points for the Archaic sample, 80 were estimated by the EM method (around 4%). No data points had to be estimated for the worldwide, comparative data set.

As a check of the accuracy of the EM method, a robust regression method for estimating missing data was also completed using SAS. In this method, the complete observations are used to construct regression matrices to estimate the

missing data. This process is repeated with several iterations until there is a high level of congruence. There was not a significant difference found between the two methods for estimating missing data. Therefore, the results shown in this dissertation are from the data with EM estimates.

Sex-standardization

Prior to any analysis, all observations were standardized within each sex as a means of eliminating sex-related size variation (Relethford, 1994; Relethford and Harpending, 1994; Williams-Blangero and Blangero, 1989) while retaining within sex size and shape variation. This was accomplished through the calculation of z-scores. The deviation of each raw measurement from the general mean of each sex is divided by the general standard deviation, so that for all the individuals' z-scores, the mean is 0.0 and the standard deviation is 1.0 (Howell, 1989). The formula is

$$z = \frac{x - \mu}{\sigma},$$

where *x* is a raw score to be standardized, μ is the mean of the sex for each measurement and σ is the standard deviation of the sex for each measurement.

Model-free analyses

The Paleoamerican, Archaic and worldwide, modern craniometric data were analyzed using a variety of model-free methods. Model-free methods can serve as an important means of data screening, exploring the dimensionality of the data and producing uncorrelated, new variables for further analysis (Johnson, 1998). Model-free analyses do *not* attempt to recover underlying population

structure present in the data; thus, these methods can explore questions regarding phenotypic variation both within and between Paleoamericans and other groups without making assumptions about the cause of any similarities or dissimilarities (Powell, 1993, 1995; Powell and Neves, 1999; Relethford and Lees, 1982). These aspects can be explored through model-bound methods.

PRINCIPAL COMPONENT ANALYSIS

Principal component analysis (PCA) is a descriptive measure that employs the pooled variance-covariance structure of the total data set, and the variance structure of the total sample is then converted to a set of orthogonal vectors, the principal components, PCs, that summarize variation in craniofacial shape (Manly, 1994; Powell and Neves, 1999). The PCs are new variables that are uncorrelated, and the first PC accounts for as much variability in the data as possible, with each succeeding component accounting for as much of the remaining variability as possible (Johnson, 1998).

PC score plots are a means of illustrating multivariate morphological relationships with no underlying assumptions. Individuals that occupy similar space in the PCA plots are morphologically similar and, at least to some degree, genetically similar under the assumption that genotypic covariance is related to phenotypic covariance in the relationship $\mathbf{G} = h^2\mathbf{P}$ (Cheverud, 1988; Konigsberg and Ousley, 1993, 1995; Williams-Blangero and Blangero, 1989). Specifically, principal component analyses were completed by eigenvalue decomposition of a data covariance matrix. A covariance matrix was chosen instead of a correlation matrix, because the decomposition is on the actual variance rather than the

standardized variance. It is more appropriate when the variables are measured on the same scale.

Four principal component analyses were conducted in this research. The first PCA considers each Paleoamerican specimen individually, and the same is true for the second PCA of the individual Paleoamericans and Archaics. The third PCA considers the Paleoamericans individually, in order to better understand the Paleoamericans' relationships with a worldwide sample, with the Archaic sample split and averaged into four groups: Midwest and Southeast North Americans and Brazilian and Colombian Archaics (see Table 6). In addition, the worldwide samples are averaged by sample. In the fourth PCA, the same criteria as the third PCA was used except the Paleoamerican sample is also split and averaged into three geographic groupings: North American, Central and South American (see Table 6). The group mean of the original variables were put into the principal component analysis.

In order to evaluate the degree of internal and external variation, group means, standard deviations and F-tests were computed. This was particularly useful when investigating whether the Paleoamericans are more internally variable than the Archaic Americans and worldwide, modern samples.

MAHALANOBIS DISTANCES

The Paleoamerican crania present difficulties that make most classical statistical approaches impractical or not ideal. Most important of these is that each specimen can be considered to be derived from a different population and

Table 6: The geographic groupings of the Paleoamerican and Archaic individuals

Geographic Groupings	Individual/ Sample
North American Paleoamericans	Arch Lake
	Browns Valley
	Buhl
	Gordon Creek
	Kennewick
	Lime Creek Burial
	Spirit Cave
	Toothpick
	West Gravel Pit (n=2)
	Wizards Beach
Central American Paleoamericans	Chimalhuacan
	C. del Tecolote
	Metro Balderas
	Penon III
	Tlapacoya
South American Paleoamericans	Cerce Grande 6 & 7 (n=5)
	Lapa Vermelha IV
	Sumidouro (n=13)
Midwest North American Archaics	Bahm Burial (n=5)
	Dry Lake (n=3)
	Fish Hatchery
	Gilder Mound
	Grant County Burial
	Medicine Crow
	Pelican Rapids
	Plattsmouth Ossuary (n=2)
	Sauk Valley
	Swanson Lake
	Trego County Burial
	Turin
	Young Burial (n=2)
Southeast North American Archaics	Windover (n=34)
Colombian Archaics	Checua (n=3)
	Chia (n=2)
	Tequendama (n=9)
Brazilian Archaics	Lagoa Santa (n=18)

n stands for sample size

are not pooled. This disallows the use of most statistical methods, which require sample sizes larger than one. Conversely, multiple crania can be pooled into a spatially and temporally unrealistic "sample," and this would allow the use of most statistical methods. Due to these difficulties, two types of Mahalanobis distance matrices are calculated.

The first matrix is useful in examining whether the individual crania resemble modern populations. This allows hypotheses to be examined regarding historical links between the Paleoamericans and more recent or extant populations (Jantz and Owsley, 2001). This can provide evidence regarding the ancestral area(s) of the first Americans. Mahalanobis squared distances between an individual Paleoamerican skull and a sample can be calculated by

$$D^2 = \left(X - X_j\right)' W^{-1} \left(X - X_j\right),$$

where X is the vector of cranial measurements for a skull, X_j is the mean vector for population j, and W is the pooled within-sample covariance matrix (Jantz and Owsley, 2001).

The second Mahalanobis distance matrix compares pooled Paleoamerican groupings to the Archaic groupings and modern, worldwide samples. Pooling crania can yield unrealistic average configurations, but whether they are unrealistic will be evaluated by comparing group standard deviations of Paleoamerican groups to modern populations. Additionally, this type of matrix should be computed in order see if similar patterns are shown as the first Mahalanobis squared distance matrix. This distance matrix was calculated in the computer program SAS.

Model-Bound Methods

Cranial distances and matrix permutation tests (Sokal et al., 1992; Waddle, 1994) are used to test the explanatory power of several theories and mechanisms that have been proposed in terms of number of migration events into the New World. Other authors have attempted similar methods focusing on these subjects with differences mainly in samples and design and distance matrices utilized (de Azevedo et al., 2011; Gonzalez-Jose et al., 2001; Hubbe et al., 2010).

Cranial distances are obtained through a Mahalanobis squared distance matrix between samples, after the modification of Williams-Blangero and Blangero (1989). Many matrices had to be computed depending on the theory being investigated in order to include the correct groupings or population per test.

Matrix permutation methodology is used to test the fit of the observed data, the biological distance matrices, with hypothetical models concerning the peopling of the Americas. These techniques were first suggested and developed by Sokal et al. (1992) to test human dispersion and settlement models for Europe. Further work by Waddle (1994) tested three models for the origin of modern *Homo* and improved matrix permutation techniques. These methods have been criticized and improved upon by Cole (1996), Konigsberg et al. (1994) and Konigsberg (1997). These suggestions are considered here.

BIOLOGICAL DISTANCES

Biological distances are assessed with a Mahalanobis generalized distances (D^2) analysis, after the modification of Williams-Blangero and Blangero

(1989). These modifications assume an additive polygenic model for the traits in which the expectation of environmental deviations is zero. D^2 represents a matrix containing the minimum genetic distances derived from the phenetic variation (Williams-Blangero and Blangero, 1989). Biological distances are given as

$$d_{ij}{}^2 = r_{ii} + r_{jj} - 2r_{ij} ,$$

where r_{ij} are the elements of an R-matrix computed for each trait in populations i and j (Relethford et al., 1997). Thus, the Mahalanobis distances and consequently the biological distance matrix are computed from elements of the R-matrix. This is an averaged distance, i.e. divided by the number of variables.

The biological distance matrix (BDM) represents the biological, observed distances or dissimilarities (d_{ij}^2) based on 17 of the Howell's craniometric variables observed in 35 samples. As noted above the number of samples utilized in each comparison differ depending on which design matrix is being compared. An equal relative population size was assumed for all groups, as these could not be accurately estimated. Distance computation and analysis of data was performed using the software RMet for Windows, version 4.0 (Relethford, 1998a), provided by J. Relethford online (http://konig.la.utk.edu/relethsoft.html).

Additionally, the second form of Mahalanobis squared distance matrix described in the previous section was also used to compare to design matrices to evaluate any differences between the two types (model-free and model-bound) of biological distance matrices. Both distance matrices are square, symmetrical matrices of dimension *N*, depending on the populations under investigation. The

two types of Mahalanobis distance matrices did not produce different results in the Mantel tests. This is expected because it is just a matter of dividing by the number of variables. The Mahalanobis generalized distances, after the modification of Williams-Blangero and Blangero (1989), comparisons are shown in the results.

SPATIAL SEPARATION

In order to test geographical patterns of cranial variation, three matrices of spatial distance were constructed. Two relatively straight-forward isolation-by-distance (IBD) models are considered here. According to a simple isolation-by-distance model, biological distance should increase with geographic distance (Wright, 1943). The first IBD model is similar to those found in other studies (de Azevedo et al., 2011; Gonzalez-Jose et al., 2001; Hubbe et al., 2011) in which great circle distances between all populations were calculated. However, the restrictions of the Bering and Panama waypoints are considered; thus, these cannot be considered the shortest routes from one point to another. Explicitly the distance between series follows terrestrial routes, considering passages across specific waypoints located in the Bering Strait and the Panama Isthmus as mandatory waypoints. Average latitudes and longitudes were computed for the Paleoamerican and Archaic groupings which are composed of a multitude of sites (all latitudes and longitudes can be found in Table 4). All distances were calculated with the use of the website http://www.movable-type.co.uk/scripts/latlong.html. This author created a simple macro program in order to impose the Bering and Panama restrictions on the distances.

Other authors have considered direct distances as “illusory” due to the fact that many would require transoceanic migrations (de Azevedo et al., 2011; Gonzalez-Jose et al., 2001); however, in order to consider other theories of migration routes into the Americas, particularly those supporting transoceanic migrations (Gladwin, 1947; Wyatt, 2004), direct great circle distances were also considered and represent the second type of IBD matrix. This matrix is an example of a true geographic distance matrix, where the elements are equal to the linear distance in kilometers between populations (Sokal, 1979). This geographic distance matrix was generated by The Geographic Distance Matrix Generator Version 1.2.3 (Ersts, 2011).

Since it is important to take into account diachronic divergence when attempting to test microevolutionary scenarios (Konigsberg, 1990), chronological variation between the populations was incorporated into the computation of distances. To test for any influence of time, each element of the IBD matrix incorporating waypoint restrictions is multiplied by the chronological difference among samples (de Azevedo et al., 2011; Hubbe et al., 2011). The chronological distances were calculated in thousands of years, taking an average when there was a chronological range in the groupings. For example, geographical distances between the recent Howells populations were multiplied by 1, the geographical distance between any modern population and North American Paleoamericans was multiplied by 9.7 (kyr BP), Central and South American Paleoamericans by 9.5 (kyr BP) and all North and South American Archaic samples by 5.3 (kyr BP).

These matrices were compared with Mantel tests to the biological distance matrix including all samples under investigation.

MATRIX PERMUTATION AND DESIGN MATRICES

Different design matrices were constructed reflecting competing hypotheses regarding the dispersion and movement of the earliest Americans into the New World in order to assess their congruence with the observed craniometric distance matrices. In a typical matrix permutation study, similarities or dissimilarities between populations are estimated after any character *observable* in the population. These are usually represented in a distance matrix. The second step is to set and describe hypothetical dissimilarities *expected* under a particular model/hypothesis. These are usually represented in design matrices and/or connection schemes (Waddle et al., 1998). The construction and evaluation of design matrices is well described in papers by Sokal et al. (1992, 1997), Waddle (1994) and Waddle et al. (1998).

Other authors have utilized matrix permutation studies in order to address questions regarding the peopling of the New World (de Azevedo et al., 2011; Gonzalez-Jose et al., 2001, 2002; Hubbe et al., 2010; Pucciarelli et al., 2008), and this analysis will attempt to compare results found here to those studies as well as develop new design matrices for ideas not covered in previous analyses. As a rule, models were kept uncomplicated, leaving the possibility for improvements. Simple models are preferable and easy to express and analyze with design matrices (Gonzalez-Jose et al., 2001).

CONNECTION SCHEMES

The design matrices are illustrated by the connection schemes that represent the four leading hypotheses focusing on the first migration(s) into the New World. A distance of zero was assumed for samples included in the same box and a value of one for samples of different but connected boxes, unless otherwise indicated. As a general rule for all models, the distance between any pair of samples of non-connected boxes was obtained by adding together the values along the path (Gonzalez-Jose et al., 2001).

Once this analysis was carried out, low correlations were recorded. In order to further analyze why there were low correlations, a variant of each of the connection schemes was additionally considered. The spatial distances, considering mandatory waypoints, of the populations are the backbone of the design matrices, and then these distances were multiplied by the appropriate number from the connection scheme. A distance of one was assumed for samples included in the same box. Adding together the values along the path provide additional multipliers.

Out of Beringia (Single Wave) Model

The Single Wave model represents a scenario of local microevolutionary differentiation *within* the Americas. This hypothesis predicts that modern Native Americans differentiated locally from earlier populations, i.e. Paleoamericans and Archaic Native Americans. There are several ways to model this hypothesis, and therefore, there will be more than one design matrix for this scenario.

The first (Figure 1) was described in Gonzalez-Jose et al. (2001) and represents a very simple model. In this scheme, samples are grouped into three boxes. The first includes the Ainu, Andaman Islands, Atayal, Easter Island, Guam, Maori, Mokapu, Moriori, Philippines and Tolai samples and represents the more generalized Sundadont dental pattern, from which typical “Mongoloids” are derived (Lahr, 1995; Turner, 1992). The second box is composed of Asian samples, which have the Sinodont dental pattern, which is a more derived dental complex typical of East and Northeast Asian populations and Native Americans. It is believed that the Sinodont morphology is derived from the Sundadont dental pattern (Turner, 1987). This box is composed of the Anyang, Buriat, Hainan, North Japan and South Japan. This box also represents the “source” for all the Americans. The third box represents the “Single Wave” and is composed of all American samples.

SW1 is a simplistic scheme representing the Out of Beringia (Single Wave) model, and a potential inaccuracy is that the “Single Wave” box represents a huge time range. SW2 (Figure 2) attempts to account for the time differences by splitting the single wave box into three while keeping the flow of the wave chronologically. This may be an important step because the sheer time span between these samples may be cause for morphological variation.

Genetic evidence has strongly suggested a single wave into the New World. As discussed in Chapter Three, two recurring observations occur with genetic evidence. Single Wave 3 (SW3), represented in Figure 3, models the first: a single ancestor group from Northeast Asia (represented by the Buriats)

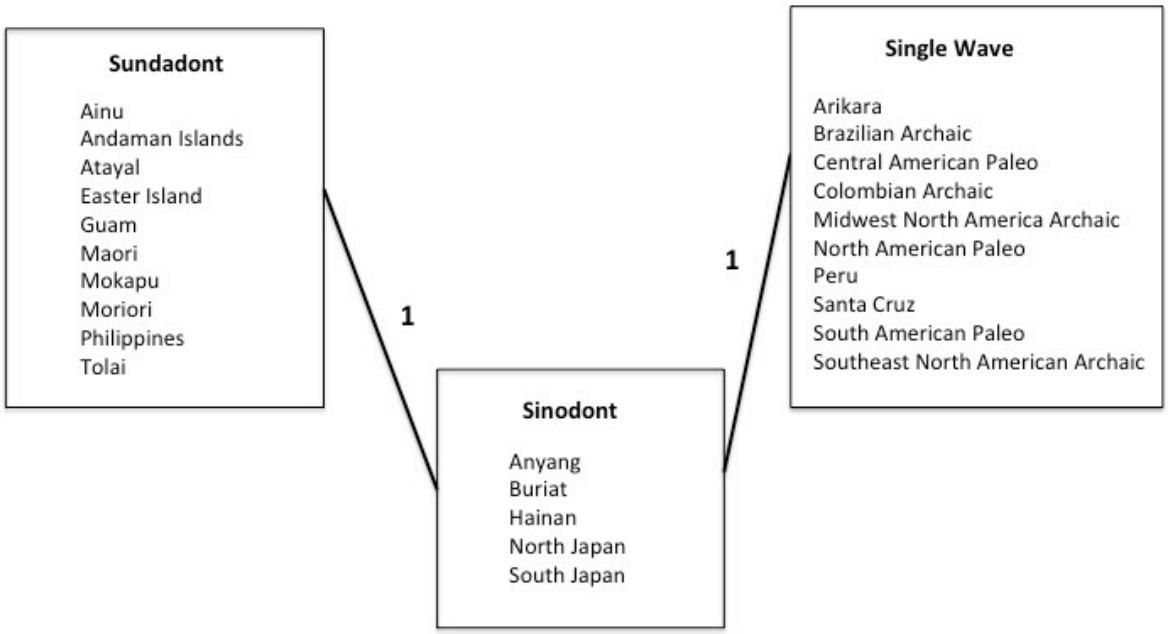

Figure 1: Single Wave 1 (SW1) connection scheme

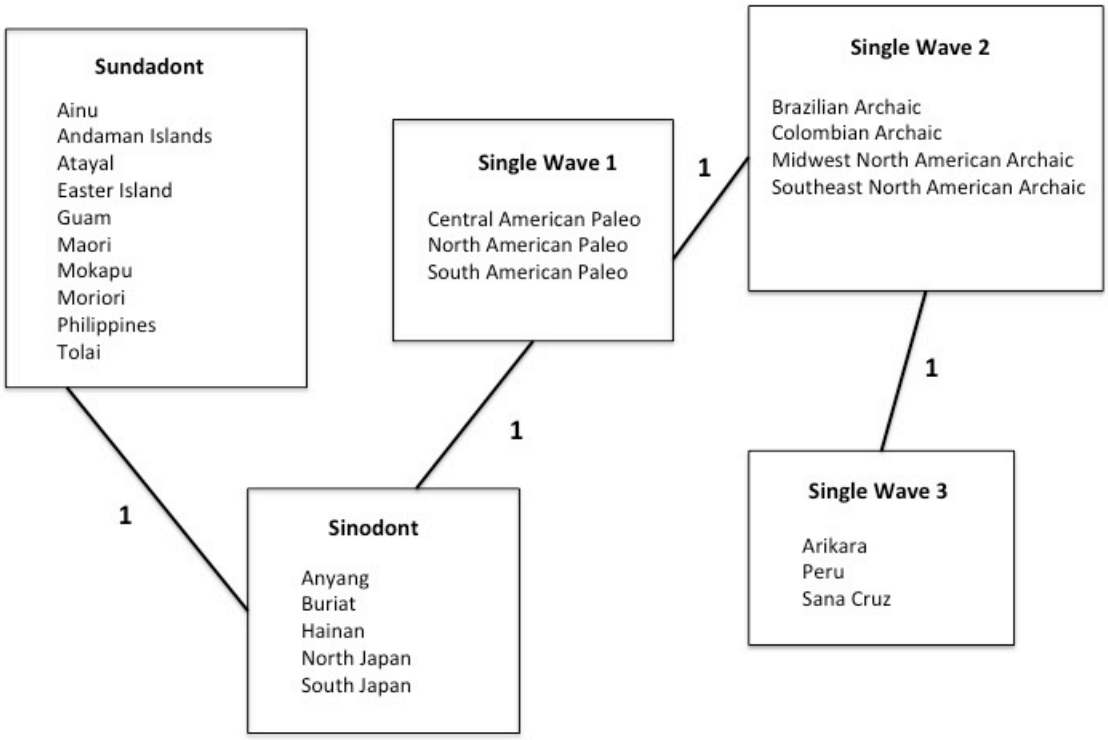

Figure 2: Single Wave 2 (SW2) connection scheme

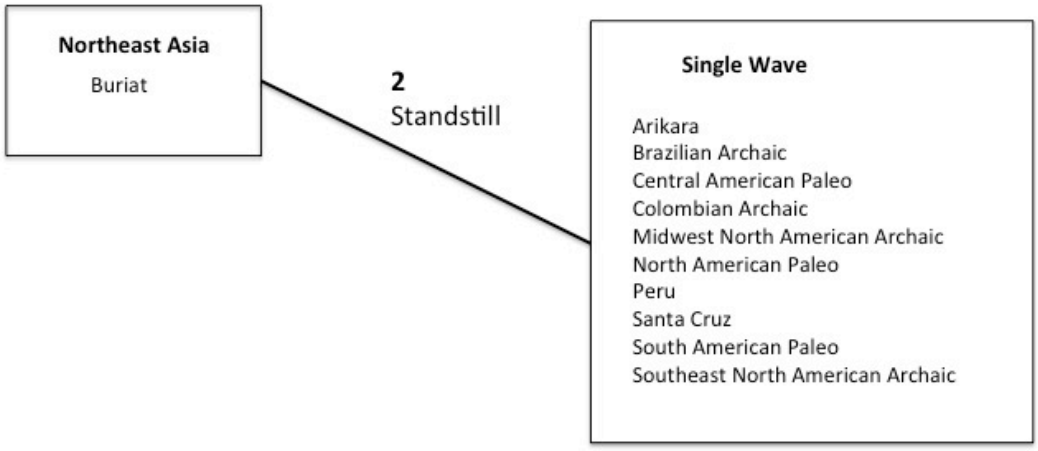

Figure 3: Single Wave 3 (SW3) connection scheme

moves into the New World in one wave after being confined in Beringia (the Beringian standstill) during the Late Pleistocene (Bonatto and Salzano, 1997 a; Fagundes et al., 2007 a,b; Tamm et al., 2007). Thus, there is a larger number, two rather than one, between the boxes.

The second recurrent conclusion of genetic evidence is modeled in Single Wave 4 (SW4): there is a molecular coalescence of most Native Americans to a unique ancestral population somewhere in eastern Asia (Bonatto and Salzano, 1997 a,b; Merriweather et al., 1995; Santos et al., 1999; Silva et al., 2002). Although this conclusion refers only to modern Native Americans, within a *single* wave framework this would include all early Americans. Refer to Figure 4 for the corresponding connection scheme.

Two Components (Two Waves) Model

The Two-Components model (TCM) was developed by Neves and Pucciarelli (1990, 1991,1998) and Neves et al. (1999a,b) and gained support from other researchers (Powell and Neves, 1999; Steele and Powell, 1992, 1993). This model argues for distinct origins for early and modern American populations, with both groups representing distinct expansion events into the continent from East Asia through Beringia.

As with the Single Wave model, several matrices were developed to test this hypothesis. The simple models are discussed first, but this theory is more complex and requires more matrices to account for possible interpretations of this model. For TCM1, the samples were divided into five boxes by geographic location and according to the divergences predicted by the Two Components

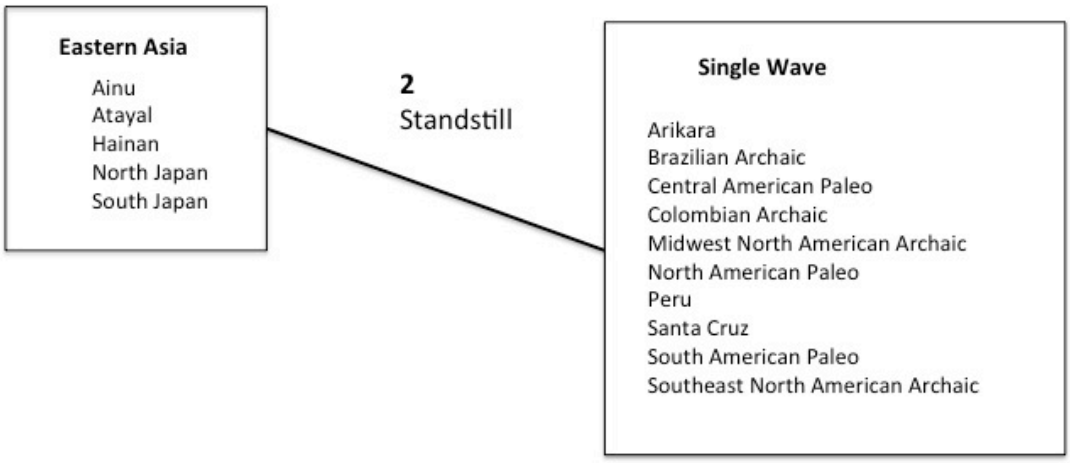

Figure 4: Single Wave 4 (SW4) connection scheme

model: Paleoamericans (North, Central and South American), Asian (Hainan, Anyang, Atayal, Buriat, N. Japan and S. Japan), most recent wave (Eskimo), Amerindian (Arikara, Santa Cruz and Peru) and Archaics (Midwest and Southeast North American, Brazilian and Colombian).

In the TCM1 scheme, as shown in Figure 5, the Asian and Amerindian boxes are connected by a small distance value (1) to indicate the predicted dispersion from a modern differentiated stock. The Paleoamerican samples are connected to the Archaic samples by the same small distance value (1) regarding their belonging to the hypothetical early wave (see TCM4 for a re-evaluation of the Paleoamerican/Archaic relationship). The Paleoamerican box is connected to the Amerindian box by a distance of 2, representing the predicted separation between a morphologically generalized modern *Homo sapiens* (early wave) and a specialized East Asian-Amerindian group. Lastly, the Eskimos were derived from the Asian stock, joining both with the minimum distance (0.5) predicted in order to represent a recent divergence. This connectivity scheme is modeled after one published in Gonzalez-Jose et al. (2001).

Gonzalez-Jose et al. (2001) also developed two modifications of their original scheme and these modifications are considered here for comparison. For TCM2, the Eskimos are derived from the Amerindian box rather than the Asian one. With TCM3, increasing the distance between Paleoamericans and Archaics from one to two, alters the triangle formed by Paleoamericans, Archaics and Amerindians.

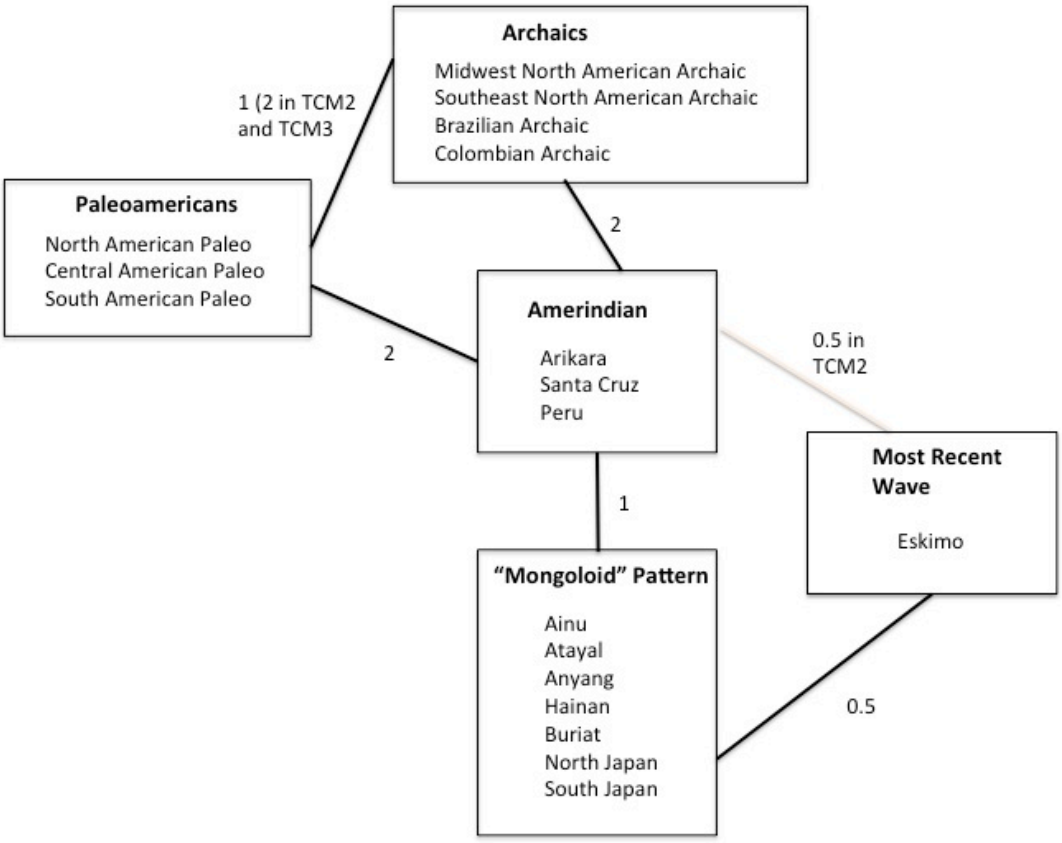

Figure 5: Two Components Model 1, 2 and 3 (TCM 1, 2 and 3) connection scheme

For TCM4, the relationship between the Paleoamericans and Archaics is reevaluated. Many of the Archaic individuals in this sample have fairly early dates, meaning that it could be appropriate for these two samples to be combined. Refer to Figure 6 for the connection scheme.

The basic tenet of the Two Components model is the assumption of two separate migrations into the New World: the first and earliest resulting in the Paleoamerican specimens and the second resulting in the modern Native Americans. The next three schemes represent this. TCM5, shown in Figure 7, is the most basic of these schemes, with the Paleoamericans descending from Sunadonts and modern Native Americans derived from populations carrying Sinodont dental traits. TCM6 combines the Paleoamerican and Archaic groups due to the early dates associated with the Archaic groups. Refer to Figure 8 for the connection scheme. TCM7, Figure 9, takes into account the possibility of interaction between Paleoamerican/Archaic individuals and individuals from the second wave that resulted in the modern Native Americans.

Tripartite (Three Waves) Model

The tripartite model was one of the first theories of the peopling of the New World to incorporate information from more than one discipline. With the use of linguistic, dental anthropology and genetics data, Greenberg et al. (1986) argued that there were three waves of migrants into the New World, and this can explain all the differences found now in the Americas. The connection scheme shown in Figure 10 is devised to describe and test this model.

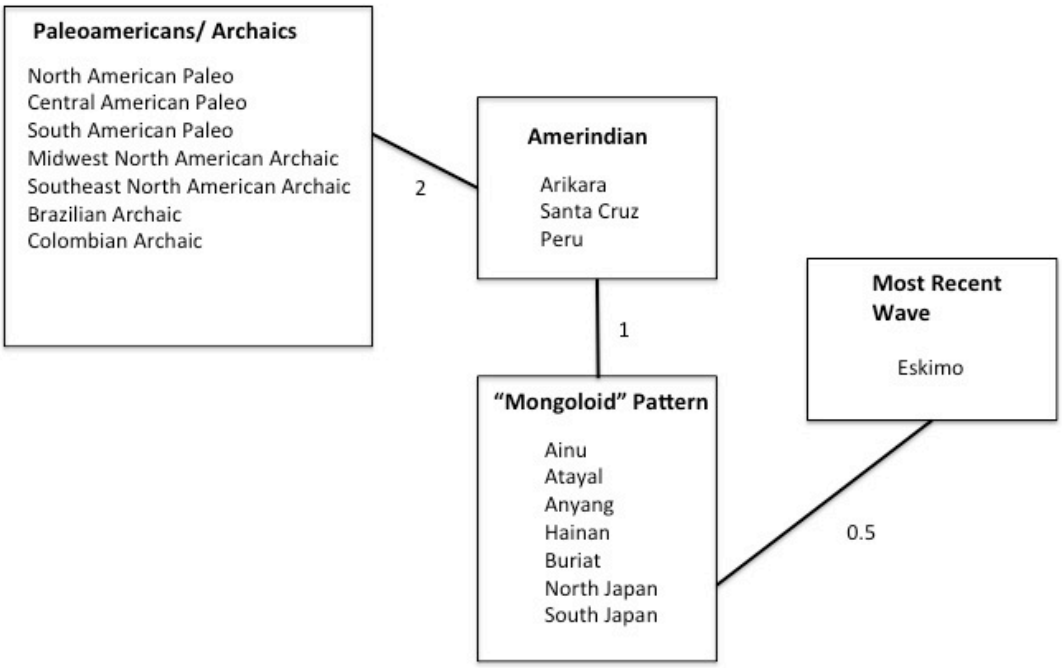

Figure 6: Two Components Model 4 (TCM4) connection scheme

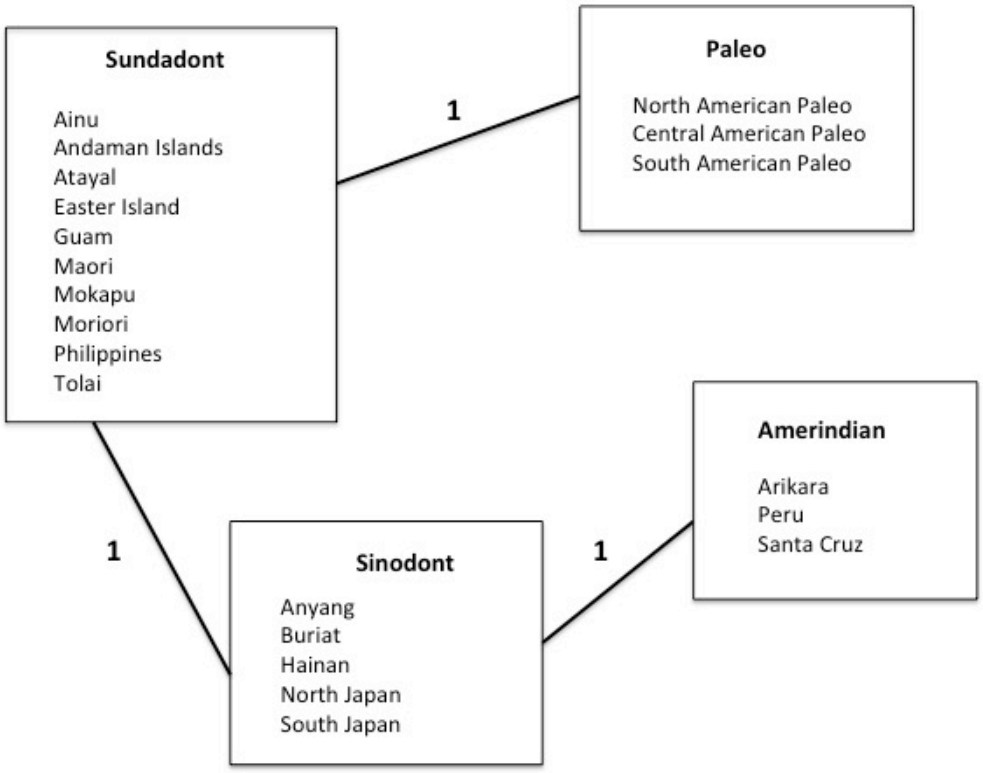

Figure 7: Two Components Model 5 (TCM5) connection scheme

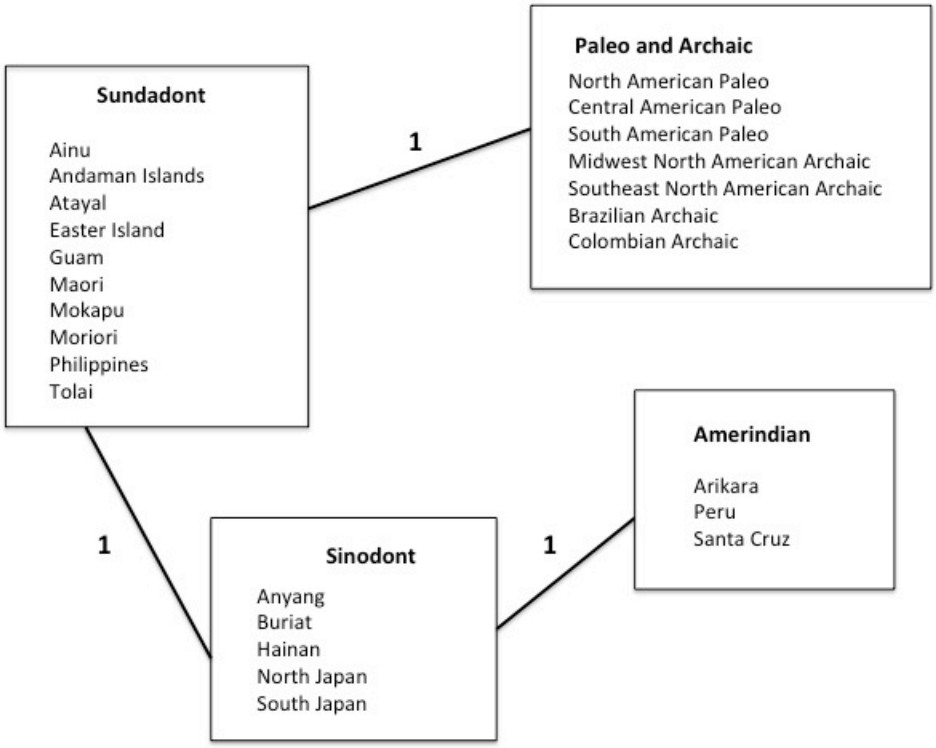

Figure 8: Two Components Model 6 (TCM6) connection scheme

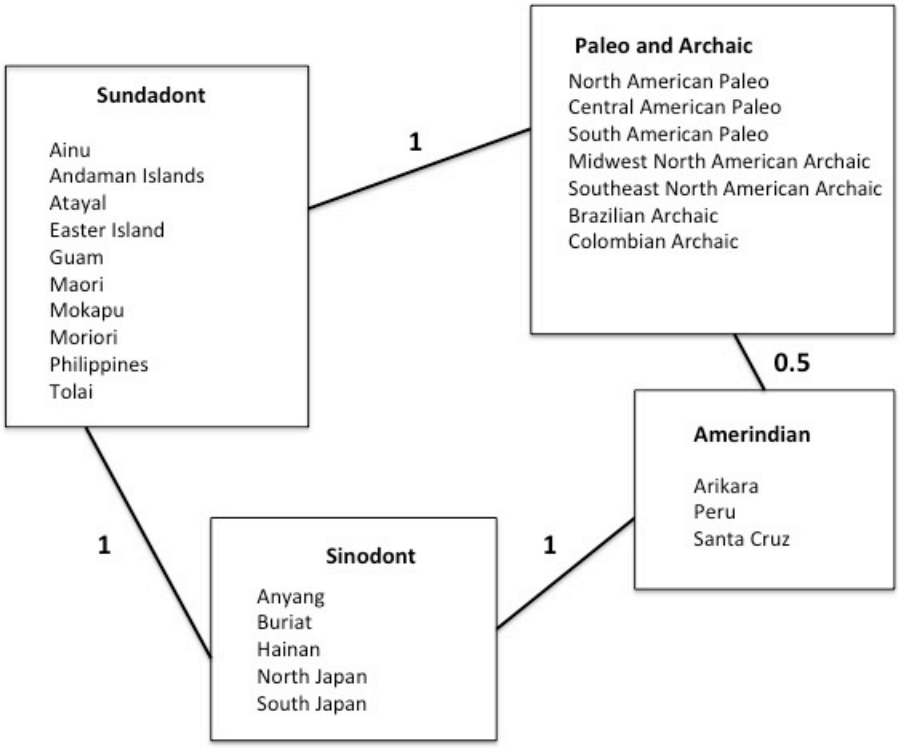

Figure 9: Two Components Model 7 (TCM7) connection scheme

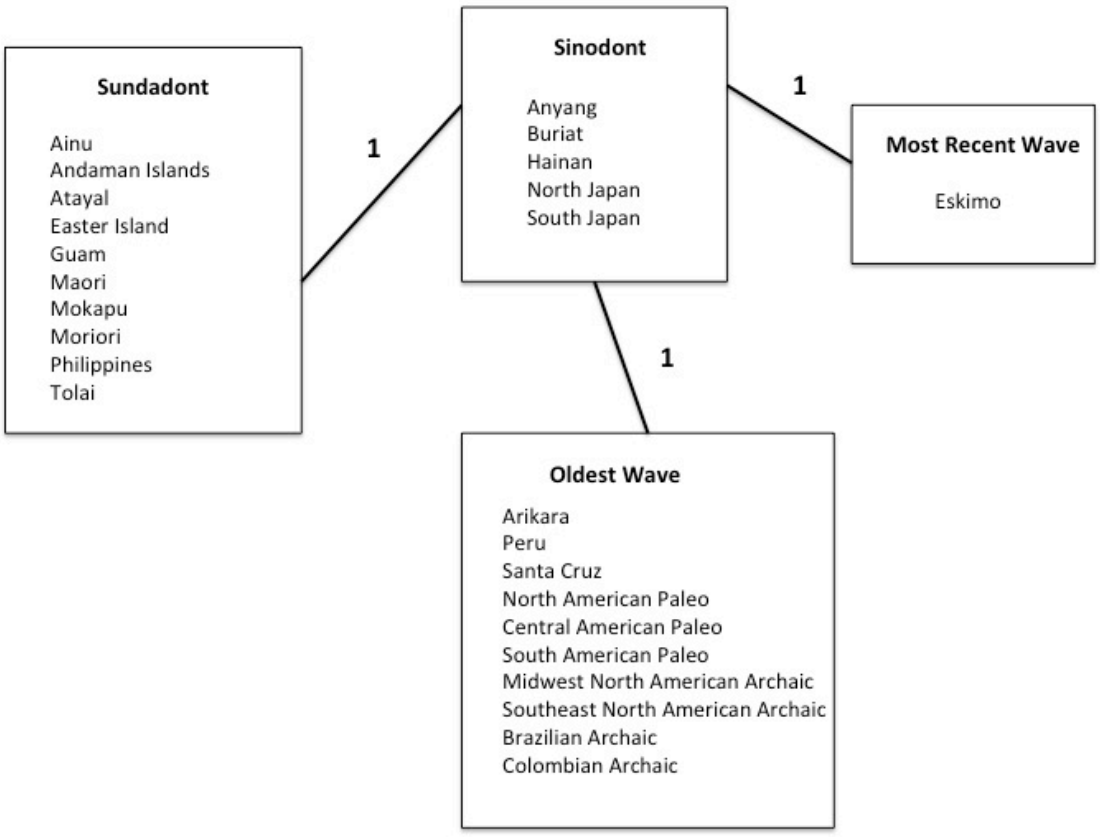

Figure 10: Three Waves Model (TWM) connection scheme

The samples are divided into four boxes and are similar to the connection scheme found in SW1. The biggest difference is a fourth box separating the Eskimo sample from the rest of the American samples in order to represent the more recent migration/division from the Asian, “Sinodont” sample. This is similar to a connection scheme described in Gonzalez-Jose et al. (2001).

Recurrent Gene Flow Model

The Recurrent Gene Flow model is more difficult to produce design matrices, because this model is still developing. Recurrent Gene Flow model 1 (RGF1), found in Figure 11, is the first attempt. Here the most important component of the connection scheme is the Arctic/circum-Arctic groups (Buriats and Eskimo), as these were the closest ancestors to the Paleoamerican group, and with recurrent gene flow from Asia, also the closest ancestors to the Archaic groups. A more systematic discussion of the Recurrent Gene Flow model is in Chapter Three.

For Recurrent Gene Flow Model 2 (RGF2), the appropriateness of the Arctic/ circum-Arctic groups is questioned in regards to representing the early founder population occupying Beringia during the last glaciation, characterized by high craniofacial diversity, founder mtDNA and Y-chromosome lineages. The Buriat and Eskimo groups are more modern and may not be appropriate for this comparison. Therefore, RGF2 connects the Paleoamerican sample directly to the Asian groups with a larger distance. The Arctic/circum-Arctic groups are also connected to the Asian groups and the Archaic groups. Refer to Figure 12 for the connection scheme.

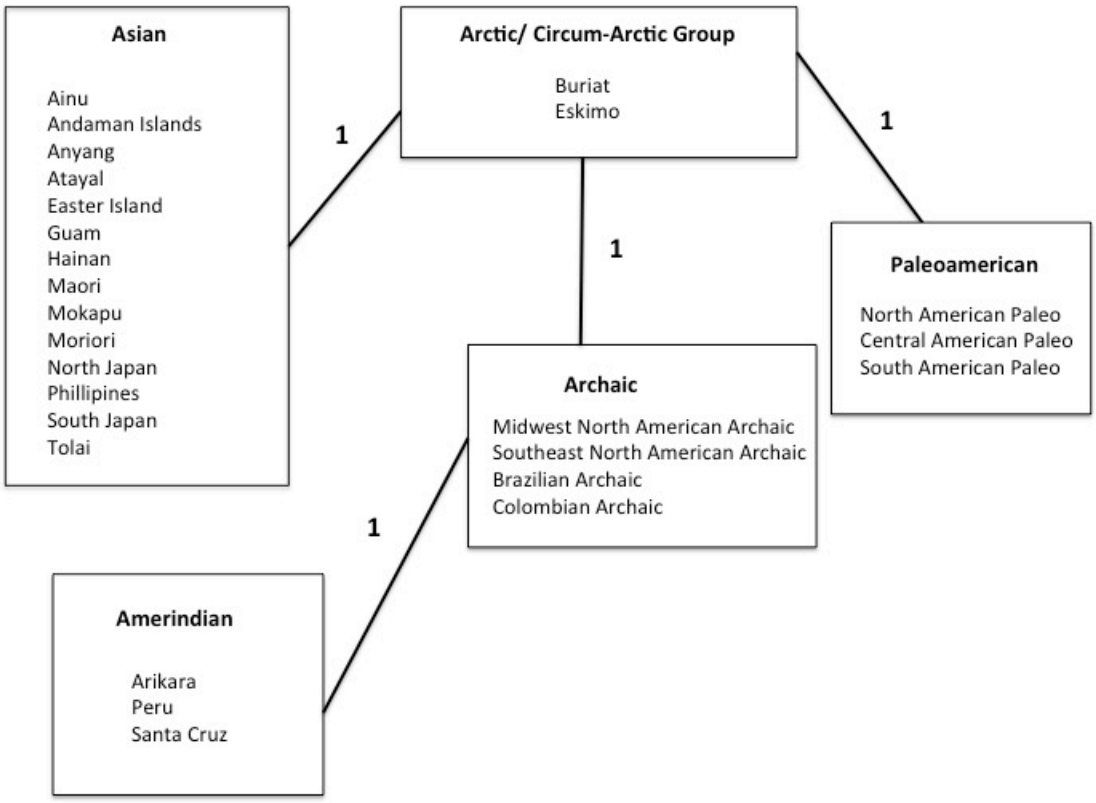

Figure 11: Recurrent Gene Flow model 1 (RGF1) connection scheme

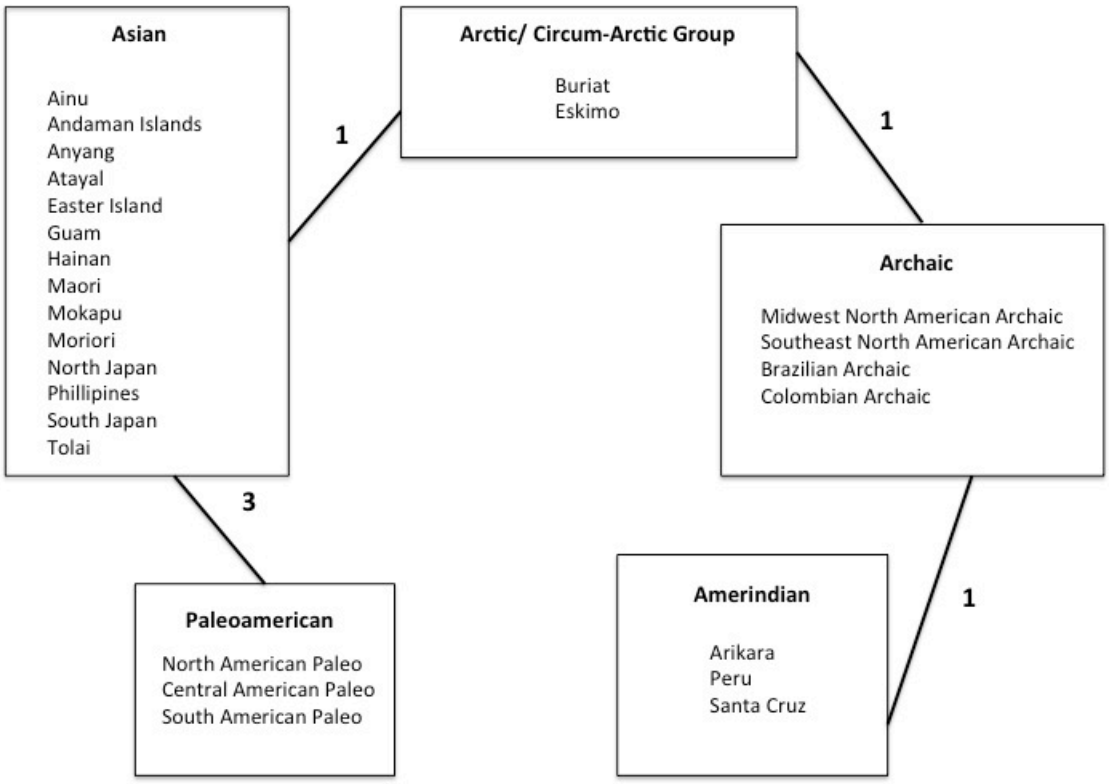

Figure 12: Recurrent Gene Flow model 2 (RGF2) connection scheme

For Recurrent Gene Flow Model 3 (RGF3), illustrated in Figure 12, there is a different consideration of the placement of the Archaic groups. The northeast Asian-derived groups dispersing into the Americas after the first migrations is unclear under the model as described by de Azevedo et al. (2011). It could have occurred concomitant with the first entry into the Americas or it could have occurred later in time. Since many of the Archaic individuals have dates close to those of the Paleoamericans, it may be more prudent to connect them with the Paleoamerican samples rather than directly to the Arctic/circum-Arctic groups. Please refer to Appendix A for the simple design matrices.

CORRELATION AMONG DISTANCE MATRICES

Mantel statistic tests (Mantel, 1967) were used to calculate correlations among the many different types of distance and design matrices, and they provide a means of testing the significance of these associations. Pearson correlation coefficients (r) measure linear dependence between two variables, which in the Mantel case represents two matrices. The coefficient ranges from -1 to 1. A value of 1 implies that a linear equation with a positive slope perfectly characterizes the relationship between two matrices, while a value of 0 implies no linear correlation. Negative values indicate that data points lie on a negatively sloped line.

Significance of the correlation was determined by a permutation test. In this test, the rows and columns of one matrix are permutated and the Mantel statistic is calculated 9999 times (Relethford, 1998b), creating a distribution that

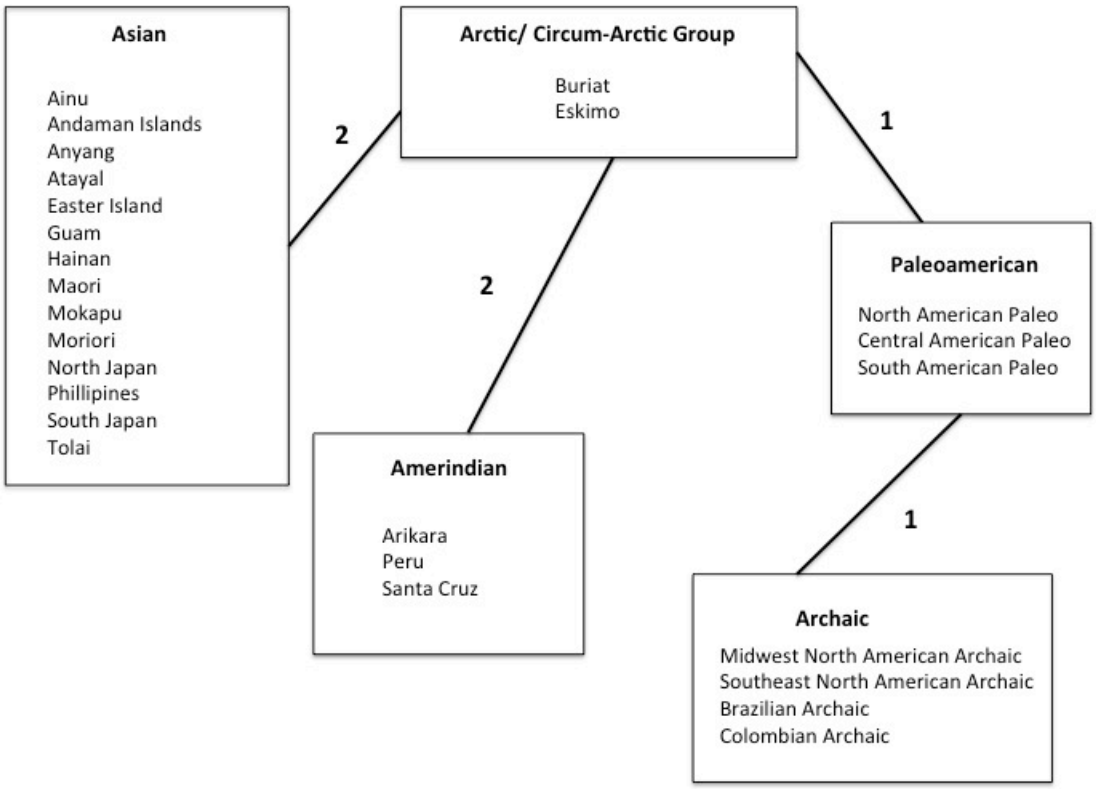

Figure 13: Recurrent Gene Flow model 3 (RGF3) connection scheme

is used to evaluate the significance of the observed correlation (Mantel, 1967; Smouse et al., 1986; Sokal and Rohlf, 1995; Waddle, 1994). All Mantel statistics were computed using the software Mantel for Windows, version 3.1 (Relethford, 1998b), provided by J. Relethford online (http://konig.la.utk.edu/relethsoft.html). Since spatial distances were considered in the design matrices, additional testing through the Smouse-Long-Sokal test (Smouse et al., 1986) was not necessary.

Chapter Six: Results and Discussion

PCA of Paleoamerican Specimens

The loading patterns of the first PCA are shown in Table 7, and the plot of the first two principal component scores for 17 sex-standardized variables across the 35 Paleoamerican individuals is presented in Figure 14. The first two components account for 50.82% of the variation in the original data. Components 1-6 have eigenvalues greater than 1 and account for 83.3% of original variation. Only the plot of the first two PCs is shown here, because this is the only one exhibiting discernable patterns.

The first principal component loadings give an indication of general cranial size differences between the Paleoamerican individuals. Most variables are positively loaded. The crania with high positive loadings for PC1 are large in terms of length and most breadth measurements considered. These include most North American and all Central American Paleoamericans. The South American Paleoamericans can be characterized as small, with a few Sumidouro exceptions, which may be an indication of notable variation in the Sumidouro subsample. The only negative loadings on PC1 are the subtenses (FRS and PAS) indicating that the large crania tend to have slightly flatter frontals and parietals.

Table 7: Loadings of the first two principal components for the Paleoamerican sample

Variable	Principal Component One	Principal Component Two
GOL	0.84896	0.29708
NOL	0.86061	0.27531
XCB	0.58418	-0.56789
XFB	0.59939	-0.64132
AUB	0.73339	-0.36596
ASB	0.53611	-0.47782
OBH	0.64988	0.37544
DKB	0.55919	0.46837
FMB	0.63145	0.52416
NAS	0.65582	0.01992
WMH	0.30727	-0.27504
FRC	0.73778	0.31985
FRS	-0.25546	0.50151
FRF	0.44214	-0.28539
PAC	0.09346	0.57176
PAS	-0.21632	0.33123
PAF	0.04225	0.53655

Table 8: Eigenvalues and Variance for Paleoamerican PCA

Number	Eigenvalue	Difference	Proportion	Cumulative
1	5.2299450	2.19613020	0.3166	0.3166
2	3.03386430	0.91790688	0.1837	0.5002
3	2.11595742	0.80474485	0.1281	0.6283
4	1.31121257	0.24191865	0.0794	0.7077
5	1.06929391	0.06663739	0.0647	0.7724
6	1.00265652	0.39436122	0.0607	0.8331
7	0.60829530	0.09758000	0.0368	0.8699
8	0.51071530	0.12921724	0.0309	0.9009
9	0.38149806	0.07690350	0.0231	0.9240
10	0.30459456	0.03099390	0.0184	0.9424

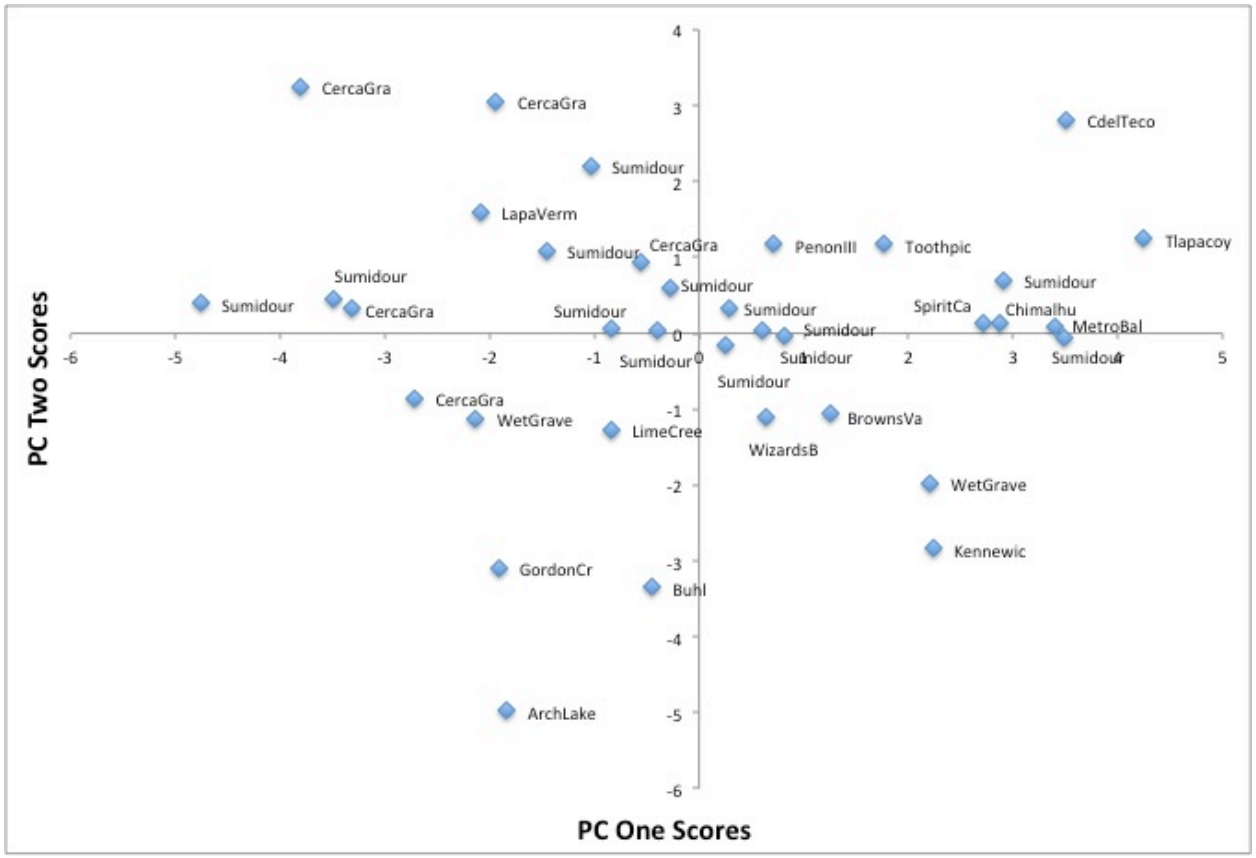

Figure 14: PCA plot of first two PC scores for individual Paleoamericans

After size is removed through PC1, the remaining principal components represent shape differences. PC2 has negative loadings for XCB, XFB, AUB and and ASB (vault measurements) as well as FRS and PAS (subtense measurements), and positive loadings for FMB, DKB and OBH (upper facial measurements). This loading pattern indicates that low PC2 scores represent individuals with relatively wide vaults, flat frontal and parietal regions and narrow upper faces, such as Arch Lake, Buhl, Gordon Creek and Kennewick (all North American). Those with high PC2 scores have the inverse of the characteristics just described, such as Cerca Grande individuals, Lapa Vermelha IV, a Sumidouro individual and Cueva del Tecolote (Central and South American).

An observation from the graph of the first two principal component scores for the Paleoamerican sample is that there appears to be variation in this sample. This is not unexpected due to the geographic and temporal differences between the individuals. There does appear to be a loose clustering of the largest subsample, Sumidouro, around the center of the chart. However, there are Sumidouro specimens on both extremes of the x-axis (PC1), indicating that there is a range in terms of cranial size. The Mexican crania also have a loose clustering separate from most of the other individuals in the upper right-hand corner of the graph. Another interesting observation is that almost all Central and South American individuals are found on the positive side of the Y-axis (PC2), and most North American Paleoamericans are on the negative side. Thus, there does appear to be separation of individuals based on phenotypic traits that also match up with geographic separation.

Table 9: Group descriptive statistics for PCs calculated from individual Paleoamerican data

Location	Statistics	Principal Component One	Principal Component Two
Central America	Mean	2.9447220	1.0924640
Central America	Stand. Deviation	1.3393043	1.1082876
North America	Mean	0.3281200	-1.7685318
North America	Stand. Deviation	1.8325204	1.7207905
South America	Mean	-0.9648926	0.7363953
South America	Stand. Deviation	2.1638527	1.0866153
	F-test (P-value)	7.96 (0.0016***)	14.54 (<0.0001***)

*** Significant at a 0.05 level

Central American Paleoamericans have the least amount of variation in principal component scores, but this may due to the low sample size (n=5). North and South Paleoamericans have higher and similar standard deviations. Based

on the f-test results, there does appear to be a significant difference between the geographic group means for PC1 and PC2.

DISCUSSION OF PCA FOR PALEOAMERICAN INDIVIDUALS

From the evidence presented in the principal component analysis and descriptive statistics on the Paleoamerican sample, there appears to be two important trends. The first is that there appears to be a notable amount of variation within the Paleoamerican sample. However, this will be better assessed when comparing to variation found within the Archaic and worldwide, modern samples. This conclusion would support previous findings (Brace et al., 2004; de Azevedo et al., 2011; Powell and Neves, 1999). This should be kept in mind when pooling of the Paleoamerican individuals is necessary in subsequent analyses; however, splitting individuals into geographic areas may help with this issue, rather than pooling into one diverse Paleoamerican group. Secondly, based on the evidence presented in Figure 14, there are phenotypic differences between the North, Central and South American Paleoamericans, which has also been suggested in Powell and Neves (1999). This may be indicative of genotypic differences as a result of different ancestral groups (i.e. different waves) or in-situ evolution occurring after a single wave.

PCA of Paleoamerican and Archaic Specimens

The loading patterns of the second PCA are shown in Table 9, and the plot of the first two principal component scores for 17 sex-standardized variables across the 35 Paleoamerican and 111 Archaic individuals is presented in Figure

15. The first two components account for 51.43% of the variation in the original data. Components 1-3 have eigenvalues greater than 1.

The PC loadings indicate that PC1 is a general indicator of size. High PC1 scores represent larger crania. Central American Paleoamericans, similar to the results of the PCA on individual Paleoamericans, are among the largest crania. However, North American Paleoamericans are no longer among the largest. In fact, they are on the intermediate or smaller end. Most South American Paleoamericans have small PC loadings and can be characterized as having smaller cranial length and breadth measurements. The Archaic samples vary within samples, with some individuals from the same group having among the highest and lowest PC1 loadings. This is particularly true for Colombian and Southeast North American Archaics. The Brazilian Archaics tend to be on the

Table 10: Loadings of the first two principal components for the individual Paleoamericans and Archaic Americans

Variable	Principal Component One	Principal Component Two
GOL	0.83048	0.37189
NOL	0.82052	0.33157
XCB	0.61739	-0.49474
XFB	0.70184	-0.43935
AUB	0.75501	-0.43997
ASB	0.62861	-0.31528
OBH	0.43414	0.16666
DKB	0.40455	0.39933
FMB	0.60215	0.18417
NAS	0.33729	-0.13237
WMH	0.47693	-0.06721
FRC	0.60894	0.25762
FRS	-0.08272	0.41506
FRF	0.56401	-0.16517
PAC	0.31623	0.76030
PAS	0.05580	0.58317
PAF	0.24162	0.65305

Table 11: Eigenvalues and Variance of PCA of Paleoamericans and Archaics

Number	Eigenvalue	Difference	Proportion	Cumulative
1	4.08763802	1.96308995	0.3351	0.3351
2	2.12454808	1.02341965	0.1742	0.5093
3	1.10112843	0.25393141	0.0903	0.5996
4	0.84719702	0.15329891	0.0695	0.6691
5	0.69389811	0.11306985	0.0569	0.7260
6	0.58082826	0.07959283	0.0476	0.7736
7	0.50123543	0.02525355	0.0411	0.8147
8	0.47598188	0.05645239	0.0390	08537
9	0.41952949	0.09889832	0.0344	0.8881
10	0.32063117	0.01103108	0.0263	0.9144

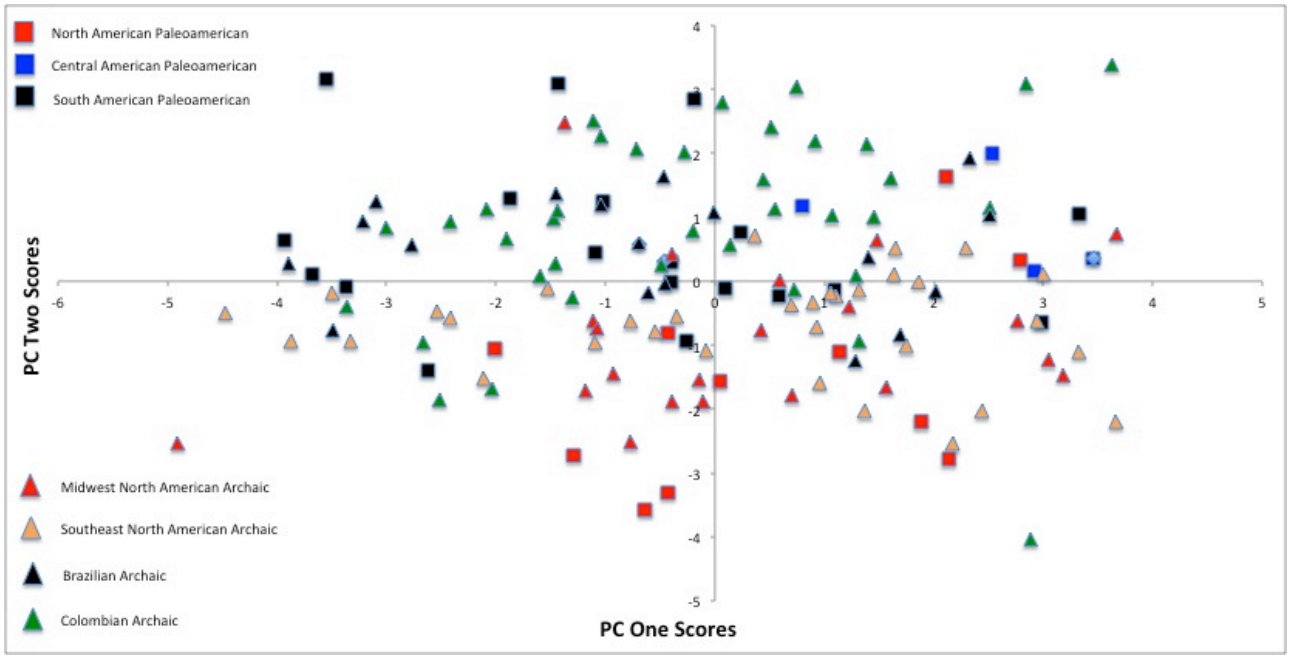

Figure 15: PCA plot of first and second PC scores of Paleoamerican and Archaic individuals

smaller side, while the Midwest North American Archaics tend to be on the larger side.

PC2 represents shape differences. The loading pattern indicates that individuals with low PC2 scores have relatively wide vaults, flat frontal and parietal regions and narrow upper faces. Most North Americans (both Paleo and Archaic) have low PC2 scores. Most Central Americans and South Americans

have high PC2 scores, implying relatively narrow vaults, frontal and parietal regions with more curvature and wider upper facial measurements.

There are a few interesting observations from the graph of the first two principal components (Figure 15). As was suggested in the PCA with just the Paleoamericans, there appears to be variation in the Paleoamerican sample but there also appears to be notable variation in the Archaic individuals. There is a separation once again between the North American and the South American Paleoamerican individuals as well as their Archaic counterparts with the North American sample found mostly on the negative side of the y-axis (PC2). The South American samples are found mostly on the positive side of the y-axis (PC2). The Central American Paleoamericans are found on the positive side of the Y-axis as well.

The group mean and standard deviation results indicate that the Paleoamerican groupings are not more internally variable than the Archaic groups. This is particularly true of the North American Archaic samples, which have high standard deviations. Additionally, the group means between geographic and temporal samples are significantly different for both principal components, as is evidenced by the F-test.

Table 12: Group descriptive statistics for PCs calculated from individual Paleoamericans and Archaics

Location	Statistics	Principal Component One	Principal Component Two
Central America Paleo	Mean	2.6325424	0.8092094
Central America Paleo	Standard Deviation	1.0977943	0.7688481
North America Paleo	Mean	0.4830833	-1.5599271
North America Paleo	Standard Deviation	1.5980068	1.5857546
South America Paleo	Mean	-0.8152811	0.5986689
South America Paleo	Standard Deviation	2.0682403	1.2873213
Brazil Archaic	Mean	-2.0109723	0.8859265
Brazil Archaic	Standard Deviation	1.3472965	0.4127999
Colombia Archaic	Mean	-0.1960405	0.8715503
Colombia Archaic	Standard Deviation	1.7552165	1.5167214
Midwest North America Archaic	Mean	-0.000782477	-0.9131137
Midwest North America Archaic	Standard Deviation	2.0661308	1.2110278
Southeast North America Archaic	Mean	0.2482989	-0.6467696
Southeast North America Archaic	Standard Deviation	2.1796585	0.7988535
	F test (P-value)	3.39 (0.0023***)	10.03 (<0.0001***)

*** Significant at a 0.05 level

DISCUSSION OF PCA OF PALEOAMERICAN AND ARCHAIC INDIVIDUALS

Perhaps the most important observation, in terms of the graph illustrating the first and second components, is that there once again seems to be a separation of North and South American Paleoamerican and Archaic samples.

This argues for the possibility of significant genetic difference between individuals residing in these continents. However, the cause of the phenotypic and presumably genotypic differences cannot be determined through this type of analysis. Possible causes include multiple migration events from different ancestral areas or in-situ evolution of phenotypic/ genotypic differences after one migration event.

Additionally, the fact that the North American Paleoamericans and Archaics are in similar PC space as well as the South American Paleoamericans and Archaics indicates phenotypic and probable genotypic similarity between these groups over time (i.e. one did not replace the other). Lastly, as was evident in the group descriptive statistics, the Archaic individuals have slightly higher levels of internal variation than the Paleoamerican individuals with significant differences between all group means.

PCA of Individual Paleoamerican, Archaic and Worldwide Samples

The loading patterns of the third PCA are shown in Table 11, and the plot of the first two principal component scores for 17 sex-standardized variables across the 36 Paleoamerican, 111 Archaic and 2410 recent, worldwide individuals is presented in Figure 16. The group means for the Archaic and modern, worldwide samples of the original variables were put into the principal component analysis. The first two components account for 51.02% of the variation in the original data. Components 1-4 have eigenvalues greater than 1 and account for 69.10% of original variation.

Table 13: Loadings of the first two principal components for the individual Paleoamerican and averaged Archaic and modern, worldwide samples

Variable	Principal Component One	Principal Component Two
GOL	0.48166	0.77198
NOL	0.51138	0.76074
XCB	0.77419	-0.31676
XFB	0.68126	-0.09856
AUB	0.93198	-0.13719
ASB	0.84089	0.04634
OBH	0.70439	-0.15022
DKB	-0.38446	0.48734
FMB	0.42758	0.74240
NAS	0.00958	0.60216
WMH	0.82894	-0.11867
FRC	0.32652	0.46722
FRS	-0.19933	0.47917
FRF	0.77642	0.05583
PAC	-0.09222	0.11712
PAS	-0.21829	0.29419
PAF	-0.36220	0.48280

Table 14: Eigenvalues and Variances of PCA for individual Paleo, Archaic and Worldwide samples

Number	Eigenvalue	Difference	Proportion	Cumulative
1	9.46063711	5.29577658	0.3388	0.3388
2	4.16486054	1.45210698	0.1491	0.4879
3	2.71275356	0.67796109	0.0971	0.5850
4	2.03479246	0.14308046	0.0729	0.6579
5	1.89171201	0.14179616	0.0677	0.7256
6	1.74991584	0.40606682	0.0627	0.7883
7	1.34384902	0.31715165	0.0481	0.8364
8	1.02669736	0.04127784	0.0368	0.8732
9	0.98541952	0.27007151	0.0353	0.9085
10	0.71534801	0.06384404	0.0256	0.9341

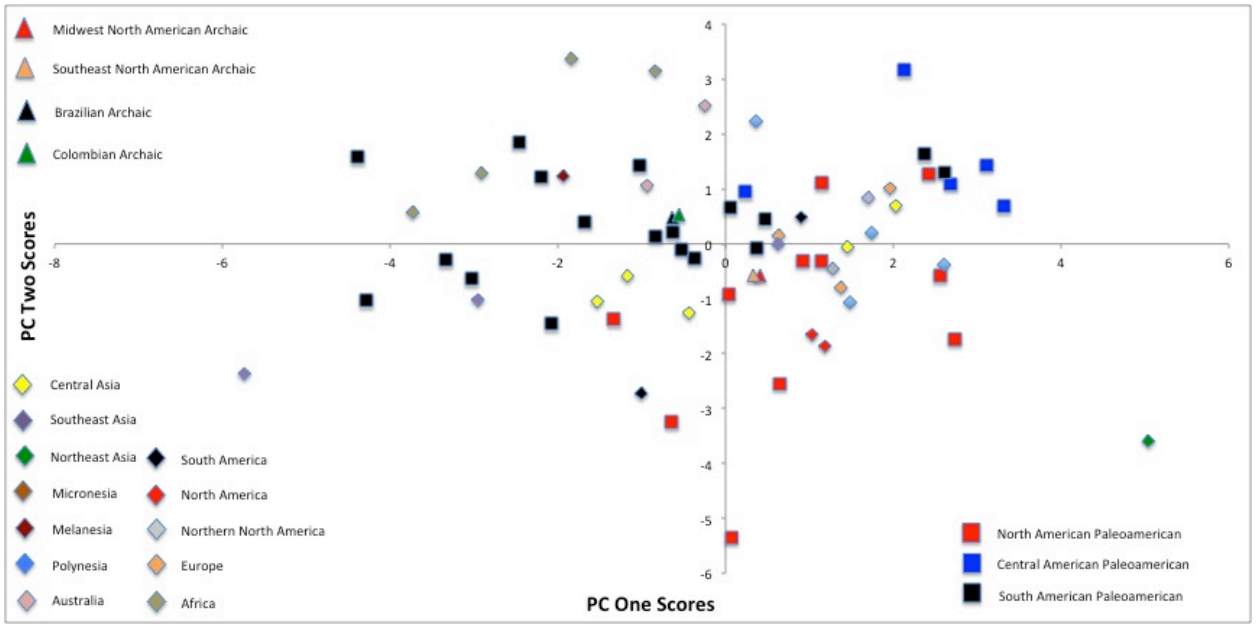

Figure 16: PCA plot of first and second PC scores of individual Paleoamericans and averaged Archaic and Worldwide groups

Based on the PC1 loading patterns, it appears that the Central and many North American crania tend to be larger in comparison to most of the averaged worldwide and archaic samples, particularly in vault breadth measurements. The Buriats, Polynesians and Europeans also have larger crania. Once averaged, the North American Archaic groups could only be considered intermediate in size. Most South American Paleoamericans have smaller crania, as well as most African and Southeast Asian groups. The second principal component scores are reflective of shape differences between the individual Paleoamericans, averaged Archaic and worldwide samples. Those with larger PC2 scores have relatively narrow crania and upper facial breadths, such as Central American Paleoamericans, some South American Paleoamericans, Africans and Australians. Smaller PC2 scores indicate relatively broader crania and upper

facial breadths. Many North American Paleoamericans and modern samples, as well as the modern Peruvian sample, have low PC2 scores.

As illustrated in the above graph, there still appears to be separation between the North, Central and South American Paleoamericans. Additionally, the geographically appropriate Archaic groupings are found in similar space as the corresponding Paleoamerican group. Interestingly, the modern North American groups, Arikara and Santa Cruz, are also relatively close to the North American Paleoamericans and Archaic, while the modern South American group, by comparison, is not as near to the earlier South American groups.

The North American Paleoamericans appear to be closest to the North American Archaics and modern samples but also share PC space with various modern eastern Asian, European and Polynesian groups. The Central American Paleoamericans are separated from most other groups but are closest to modern European and eastern Asian groups. Lastly, the South American Paleoamericans share similar space to South American Archaic groups and modern African, Melanesian and Australian groups.

The most important observation obtained from the group descriptive statistics (Appendix B) for all samples under investigation is that the Paleoamerican geographic groupings are not more variable than any other group. In fact, they appear to be less variable than many modern or Archaic groupings. This is contradictory to conclusions put forth in other studies focusing on this topic (Brace et al., de Azevedo et al., 2011; Powell and Neves, 1999).

There is a significant difference between the group means for both PC1 and PC2 as shown in the F tests.

DISCUSSION OF PCA FOR INDIVIDUAL PALEOAMERICANS AND AVERAGED ARCHAICS AND WORLDWIDE GROUPS

In the graph of PC1 and PC2, there are two noticeable patterns, which are similar to previously discussed PCAs. The first pattern is geographically similar Paleoamerican and Archaic groupings sharing PCA space and in the case of North Americans, the modern worldwide samples. This provides an argument for genotypic similarity of these groups through time. These similarities are investigated more using model-bound methodology.

Secondly, there are notable phenotypic similarities between the North American Paleoamericans and modern Polynesian, eastern Asian and European groups. Additionally, the PC graph shows that the South American Paleoamericans share phenotypic similarities with modern African and Southeast Asian groups. Central American Paleoamericans have phenotypic similarities with European and eastern Asian groups. These similarities may be indicative of genotypic similarities, suggesting an ancestral relationship. Other factors could be the cause of the phenotypic similarities, such as adaptation to similar environments, climates or diets. This is further examined through Mahalanobis distances and model-bound methods.

The group mean and standard deviation results for all groups reveals that the Paleoamerican groupings do not show a higher degree of internal variation in comparison to other worldwide or temporal groupings; in fact, they appear to be

less variable than many other samples. This is contradictory to results presented in other investigations (Brace et al., 2004; de Azevedo et al., 2011; Powell and Neves, 1999). This could be the result of different statistical procedures utilized, different interpretation of results and different samples and sample sizes.

PCA of Averaged Paleoamerican, Archaic and Worldwide Samples

The plot of the first two principal component scores for 17 sex-standardized variables across the 36 Paleoamerican, 111 Archaic and 2410 recent, worldwide individuals is presented in Figure 17. In order to further investigate possible ancestral areas, all samples or groupings were averaged. The group means of the original variables were put into the principal component analysis. The first two components account for 51.11% of the variation in the original data. Components 1-4 have eigenvalues greater than 1 and account for 77.43% of original variation. The loadings are not presented here because they are similar to those shown for the individual Paleoamericans and averaged Archaic and worldwide samples, and thus, the interpretations are the same.

As was shown in the previous PCA analyses, the North and South Paleoamericans are very close to their geographically corresponding Archaic groups. This is even more obvious here with the Paleoamerican individuals averaged and some of the diversity is lost. Additionally, the North American modern groups are in close PC space with the North American Paleoamericans and Archaics. The South American modern group (Peru) is not close to the South American Paleoamericans and Archaics. The Peruvian group is not particularly

Table 15: Eigenvalues and Variances of PCA of averaged Paleo, Archaic and Worldwide

Number	Eigenvalue	Difference	Proportion	Cumulative
1	4.99567009	2.16207608	0.3573	0.3573
2	2.83359402	1.19464673	0.2027	0.5600
3	1.63894728	0.37327374	0.1172	0.6772
4	1.26567355	0.37175071	0.0905	0.7677
5	0.89392283	0.21953190	0.0639	0.8316
6	0.67439093	0.13697131	0.0482	0.8799
7	0.53741962	0.16255768	0.0384	0.9183
8	0.37486193	0.12940423	0.0268	0.9451
9	0.24545770	0.06364576	0.0176	0.9627
10	0.18181194	0.01922036	0.0130	0.9757

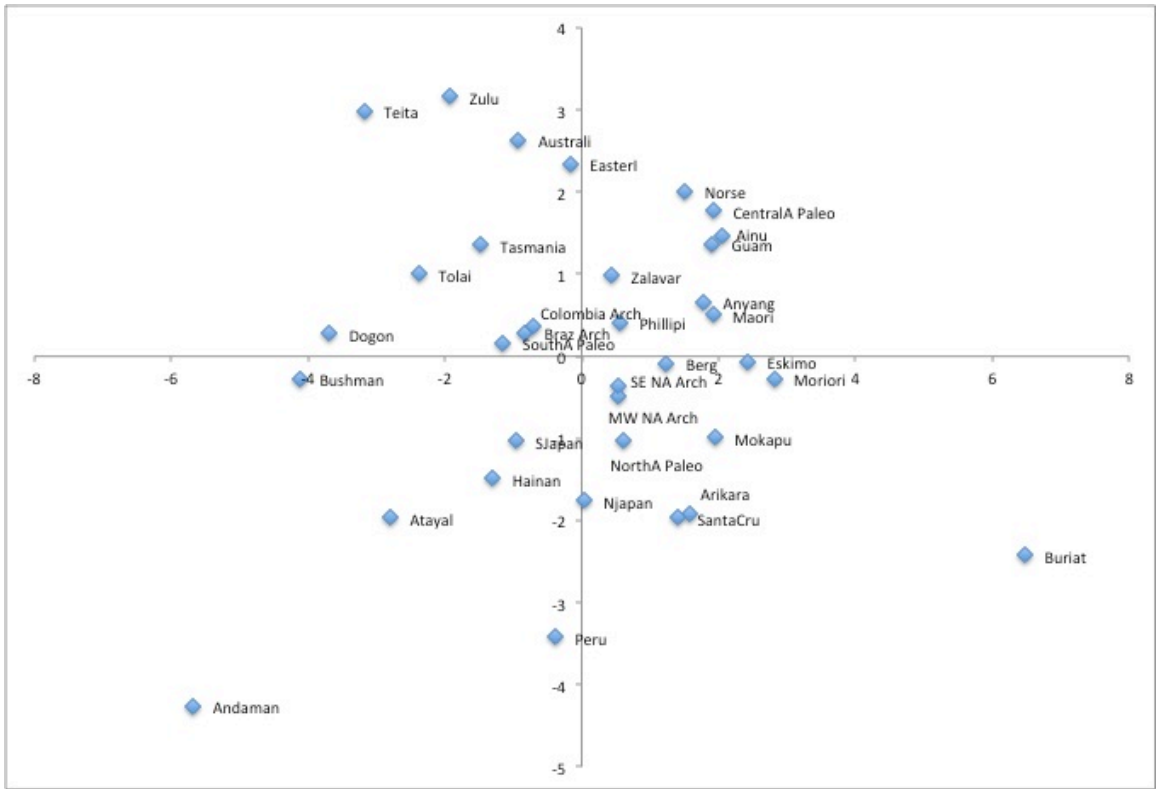

Figure 17: PCA plot of first and second PC scores of averaged Paleoamericans, Archaics and Worldwide groups

close to any group. In terms of possible ancestral areas, the North American Paleoamericans are closest to eastern Asian and Europeans. The South American Paleoamericans are not very close to any other modern groups, while being closest to the South American Archaic groups. With the Central American Paleoamericans averaged, they are more intertwined with the other groups, yet they still are found on the outskirts of the plot. They are closest to a European, eastern Asian and Polynesian groups. Mahalanobis distances will be used to see if these patterns are found in more than one type of analysis.

DISCUSSION OF PCA FOR AVERAGED PALEOAMERICANS, ARCHAICS AND WORLDWIDE GROUPS

Through interpretations of the various principal component analyses, there does not appear to be a strong, straightforward association between any Paleoamerican group and a particular ancestral area. However, all three Paleoamerican groups are in proximity to at least one eastern Asian group. Since there are phenotypic similarities between the Paleoamerican groupings and the eastern Asian groups, this may be an indication that there is a genetic relationship and thus may be a possible ancestral area for all Paleoamericans. Further analysis using other statistical methods may provide additional evidence of this.

OVERALL OBSERVATIONS FROM PRINCIPAL COMPONENT ANALYSIS AND GROUP VARIANCE ANALYSIS

There are four main observations or noticeable trends from the various principal component and group variance analyses. (1) The first observation is that the Paleoamerican and Archaic individuals from similar geographic areas also share similar PCA space. Individuals that occupy similar space in the PCA plots are morphologically similar and are considered to be, at least to some degree, genetically similar under the assumption that genotypic covariance is related to phenotypic covariance in the relationship $\mathbf{G} = h^2\mathbf{P}$ (Cheverud, 1988; Konigsberg and Ousley, 1993, 1995; Williams-Blangero and Blangero, 1989). Thus, this is evidence of genetic relationships between the earliest Americans and subsequent populations residing in similar geographic areas. In the case of North American individuals, there appears to be phenotypic continuity from Paleoamericans to modern Native Americans. However, this does not appear to be the case in South America, although the modern South Americans are only represented by one sample (Peru). These results do not support the arguments put forth by the Two Components model of migration and supports the Single Wave or Recurrent Gene Flow models. As described in the isolation by distance model (Wright, 1943), biological distance should increase with geographic distances. Thus, the geographic proximity of these groupings could be a factor in their close biological distances, but the temporal differences indicate that there must be other explanations, such as genotypic similarities, for the phenotypic similarities.

(2) The second observation from the principal component analyses is that eastern Asian populations are found in similar PCA plot space for all three Paleoamerican groupings. This is evidence for a possible eastern Asian origination point for the earliest American settlers. However, other worldwide populations are also found in proximity to the Paleoamericans, and they differ in respect to geographic Paleoamerican groupings. This observation is evaluated more through Mahalanobis distances.

(3) Although there appears to be phenotypic similarities between geographic counterparts (i.e. North American Paleoamerican, Archaic and modern samples, etc…), there does not appear to be much phenotypic and presumably genotypic similarity between the Paleoamerican geographic groupings. In particular, the North and South Paleoamericans are almost always found in different areas of the PCA plots. Additionally, the Central American Paleoamericans do not appear to be in an intermediate position between the North and South American Paleoamericans. This can be construed as evidence against the Single Wave model, assuming in-situ evolution was not a significant factor, because all Paleoamericans are not phenotypically and presumably genotypically similar (i.e. descended from one wave). However, it could be evidence for the Recurrent Gene Flow model, which posits that the single ancestral wave was diverse both craniofacially and genetically (de Azevedo et al., 2011).

(4) Lastly, as is shown through group means and standard deviation analyses, the Paleoamerican groupings are not more internally variable than the

Archaic Native American and worldwide, modern samples. This is contradictory to conclusions published in various studies, in particular the influential paper by Powell and Neves (1999). Different samples as well as different statistical procedures were utilized to come to this conclusion.

Mahalanobis Squared Distance Matrix of Individual Paleoamericans and Archaic and Modern, Worldwide Samples

Table 12 shows the five lowest Mahalanobis squared distances for the Paleoamerican specimens. For all of the Paleoamerican individuals and samples, one of the top five groups consists of an Archaic sample or a modern, Native American population. This supports the findings of the principal component analyses, which indicates phenotypic and presumably genotypic similarity between these samples. Another interesting observation is that all but three, Browns Valley, Lime Creek and the West Gravel Pit sample, of the North American Paleoamericans individuals have at least one modern, European sample in their top five. In many cases, more than one or all three European samples are among the lowest distances. Eastern Asian samples also have low distances for six out of the ten North American Paleoamericans. Polynesian and Northeast Asian samples are also among the lowest distances for some of the North American Paleoamericans.

Table 16: Results derived from Mahalanobis distance matrix of individual Paleoamerican, Archaic groupings and modern, worldwide populations

Paleoamerican	Smallest Distance	2nd	3rd	4th	5th
Arch Lake	Berg (73.082)	Buriat (75.123)	Peru (84.152)	Zalavar (88.836)	Norse (91.353)
Browns Valley	Arikara (28.663)	Maori (32.601)	Santa Cruz (33.986)	Moriori (34.373)	SE North American Archaic (35.235)
Buhl	Arikara (24.331)	Zalavar (26.395)	SE North American Archaic (27.434)	Ainu (27.660)	Berg (27.677)
Cueva del Tecolote	Maori (41.778)	Moriori (43.232)	Easter Island (43.476)	Mokapu (45.433)	Colombian Archaic (48.193)
Chimalhuacan	Santa Cruz (15.333)	Ainu (15.808)	North Japan (16.961)	Norse (17.611)	MW North American Archaic (19.016)
Gordon Creek	Zalavar (18.497)	Buriat (19.563)	Berg (20.151)	Ainu (20.628)	SE North American Archaic (20.991)
Kennewick	SE North American Archaic (33.542)	Peru (40.282)	Arikara (41.919)	Norse (43.445)	Zalavar (44.492)
Lapa Vermelha	Teita (20.137)	Eskimo (21.636)	Bushman (22.095)	Zulu (22.234)	Tolai (22.860)
Lime Creek	Santa Cruz (19.862)	North Japan (20.622)	Peru (22.820)	Ainu (22.989)	Eskimo (23.468)
Metro Balderas	Moriori (21.579)	MW North American Archaic (25.010)	Mokapu (25.333)	Arikara (26.069)	Norse (27.376)
Penon III	Anyang (11.931)	Hainan (11.970)	Guam (12.313)	South Japan (13.631)	Colombian Archaic (15.401)
Spirit Cave	Norse (14.404)	Zalavar (16.482)	Berg (19.339)	Ainu (19.580)	MW North American Archaic (20.899)
Sumidouro	Colombian Archaic (2.891)	Philippines (3.081)	Brazilian Archaic (3.591)	North Japan (3.979)	South Japan (4.263)
Tlapacoya	Mokapu (40.464)	Colombian Archaic (50.913)	Moriori (52.240)	Maori (55.442)	Easter Island (55.786)
Toothpick	Norse (18.026)	Ainu (18.260)	Colombian Archaic (19.845)	Zalavar (21.345)	South Japan (22.060)
West Gravel Pit	MW North American Archaic (12.489)	Hainan (16.049)	Peru (16.801)	Moriori (17.932)	Guam (18.095)
Wizards Beach	Arikara (10.865)	MW North American Archaic (13.275)	Moriori (13.526)	Peru (14.569)	Norse (17.156)

For the Central American Paleoamericans, Polynesian samples predominate the lowest Mahalanobis squared distances for all but one (Chimalhuacan). This is especially true for Cueva del Tecolote and Tlapacoya, where four out of the top five are Polynesian samples. Eastern Asian and European samples are also found to have low distances for Central American Paleoamericans. The South American Paleoamericans also have Polynesian and eastern Asian samples among their lowest distances. Interestingly, the Lapa Vermelha IV individual has three African samples among its lowest distances.

Mahalanobis Squared Distance Matrix of Paleoamerican Groupings and Archaic and Modern, Worldwide Samples

Table 13 shows results derived from a Mahalanobis squared distance matrix of Paleoamerican groupings and Archaic and modern, worldwide samples. The full table can found in Appendix C. The results are similar to those of the individual Paleoamerican Mahalanobis squared distance matrix. All Paleoamerican groupings have at least one Archaic and/or modern Native American sample within the ten lowest distances. The Central American Paleoamerican grouping has Polynesian and eastern Asian populations among its lowest distances. The North American Paleoamericans have European, eastern Asian and a Polynesian sample among its lowest distances. Lastly, the South American Paleoamericans have Polynesian, eastern Asian and African populations among their lowest distances. The fact that the same geographic areas represent the lowest distances in the individual Paleoamerican and pooled

Table 17: Results drawn from Mahalanobis squared distance matrix of Paleoamerican and Archaic groupings and modern, worldwide populations

Central American Paleo	North American Paleo	South American Paleo
Moriori (7.017)	Arikara (6.628)	Colombian Archaic (2.459)
Mokapu (7.540)	Zalavar (8.662)	Brazilian Archaic (3.125)
Colombian Archaic (9.430)	MW North American Archaic (8.967)	Atayal (4.055)
Maori (10.097)	SE North American Archaic (8.989)	North Japan (4.912)
North Japan (11.031)	Santa Cruz (9.886)	Philippines (4.921)
South Japan (12.829)	Berg (10.347)	Guam (5.758)
Guam (13.271)	Ainu (11.305)	Ainu (5.945)
Brazilian Archaic (13.615)	South Japan (13.194)	Bushman (6.590)
Ainu (13.890)	Moriori (13.685)	Hainan (7.365)
Arikara (15.619)	Hainan (14.255)	Dogon (7.678)

Paleoamerican Mahalanobis squared distance matrices is promising for finding trends or possible ancestral areas of the earliest Americans.

DISCUSSION OF MAHALANOBIS SQUARED DISTANCE MATRICES

There are five main observations relating to ancestral area(s) of the earliest Americans from the Mahalanobis distance analyses. (1) The first observation is that for both distance matrices Archaic and modern American samples are found to have among the lowest distances for both individual Paleoamericans and pooled Paleoamerican groupings. This is evidence of phenotypic and genotypic similarity among temporally different American groups and argues against the complete replacement of the earliest migrants by later American groups. This can be viewed as support for the Single Wave and Recurrent Gene Flow hypotheses and against the Two Components and Three Wave models for migration into the New World. Additionally, these results are similar to those presented in the various principal component analyses.

(2) Secondly, Southeast Asian and Polynesian groups are found among the lowest distances for all pooled Paleoamerican groupings and most individual Paleoamericans. This is particularly true for Central and South American Paleoamericans. (3) A third observation is that eastern Asian populations are also among the lowest distances for all pooled Paleoamerican groupings and most individual Paleoamericans. This supports findings of the principal component analyses. These observations support the hypotheses of a Southeast Asian/Polynesian or eastern Asian origination point for all of the earliest Americans. There is not stronger evidence for one area over the other through this form of analysis.

(4) European samples are commonly among the lowest distances for the North American Paleoamerican pooled grouping as well as the individual North American Paleoamericans. This is evidence for a possible European ancestral area for North American Paleoamericans or similar adaptations, which resulted in similar phenotypic traits, for North American Paleoamericans and modern, European populations. (5) Lastly, African populations are among the lowest distances for the South American Paleoamerican pooled grouping as well as the individual South American Paleoamericans. This is evidence for either a possible African origination point for South American Paleoamericans or similar adaptations, which resulted in similar phenotypic traits, for South American Paleoamericans and modern, African populations.

Model-Bound Results and Discussion

MANTEL STATISTICS

Mantel pairwise correlations between the complete (i.e. including all populations) biological distance matrix (BIO) and the three spatial matrices were calculated and are presented in Table 14.

Table 14 shows that there is correlation between all of the spatial/ temporal matrices and the biological distance matrix. However, only the spatial matrices are significantly correlated. This indicates that geography should be taken into account in the design matrices.

Pairwise correlations between the various biological distance matrices (BIO) and the 15 design matrices (SW1, SW2, SW3, SW4, TCM1, TCM2, TCM3, TCM4, TCM5, TCM6, TCM7, TWM1, RGF1, RGF2 and RGF3) are given in Table 15. Both versions of the design matrices (simple and geographic-based) were tested but the results did not vary significantly. The results of the simple design matrices are shown here.

Table 18: Results of Mantel tests between the full biological distance matrix and three spatial matrices

Spatial Matrix	Correlation (P-value)
IDB considering waypoints	0.3114 (0.0031)***
Actual IDB	0.1786 (0.0010)***
IDB with time consideration	0.1121 (0.0567)

*** Significant at the 0.05 level

Table 19: Results of Mantel tests between the various biological distance matrices and design matrices

Design Matrix	Correlation	P-value
SW1	-0.0283	0.7740
SW2	-0.1188	0.9040
SW3	***0.5566***	***0.0090******
SW4	-0.0448	0.3570
TCM1	0.0693	0.2910
TCM2	0.0631	0.3870
TCM3	0.0679	0.3480
TCM4	0.0591	0.2690
TCM5	-0.0109	0.3660
TCM6	-0.0536	0.4980
TCM7	-0.0077	0.3430
TWM	0.0473	0.4270
RGF1	-0.0655	0.6080
RGF2	0.0110	0.3310
RGF3	-0.0907	0.7180

*** Significant at the 0.05 level

As is indicated in the table above, only Single Wave model 3 is significantly correlated with its corresponding biological distance matrix. Other than SW3, the correlations are uniformly low and non-significant.

DISCUSSION OF THE MODEL-BOUND RESULTS

Single Wave model 3 is the only design matrix to be significantly correlated with its biological distance matrix. This model represents one of the two recurring observations of genetic evidence: a single ancestor group from Northeast Asia (represented by Buriats) moved into the New World in one wave after being confined in Beringia (the Beringian standstill) during the Late Pleistocene (Bonatto and Salzano, 1997 a; Fagundes et al., 2007 a,b; Tamm et al., 2007). This single migration resulted in all native Americans (Paleoamericans, Archaic and modern). This lends support to the Single Wave theory of first movements into the New World.

However, there are several problems with the SW3 design matrix. The most important of these is that only one population represents Northeast Asia: the Buriats. The Buriats, as indicated in the various PCAs, is a clear outlier. They have very large and wide crania. Since this is the only population included for Northeast Asia it may not be an accurate representation of individuals in this area. More Northeast Asian populations would better evaluate the appropriateness of the Buriats as a fair representation of Northeast Asian characteristics. Additionally, the observation from genetic research that SW3 is modeling argues that there was an ancestor group coming from Northeast Asia; however, this does not necessarily mean that the ancestors originated in Northeast Asia but merely that they left from this area before moving into the Americas. Thus, there are improvements that could be made to SW3, as with many of the design matrices.

Another interesting result from the Mantel pairwise correlation tests on the design matrices is that other comparisons had uniformly low and non-significant correlations. This can mean one of two things. The first is that the other models or variants of models do not accurately describe the way in which the first migrants moved into the New World. In other words, these models are incorrect. However, there may be other explanations for these low correlations.

Other studies have found significance using similar design matrices. In particular, Gonzalez-Jose et al. (2001) found higher correlations with similar design matrices for Two Components models but did not report significance tests. de Azevedo et al. (2011) found significant correlations with similar design

matrices for Recurrent Gene Flow models. All three analyses, this dissertation included, utilized different data sets with Gonzalez-Jose et al. (2001) heavily skewed towards South American data and de Azevedo et al. (2011) also skewed towards South American data but including an additional Late Pleistocene (Early) Old World sample. This dissertation utilizes a large Paleoamerican sample including North, Central and South American individuals but no Late Pleistocene (Early) Old World sample. Additionally, a large North American Archaic sample was included, in addition to South American Archaic samples. One can conclude that significance between design matrices and biological distance matrices is highly dependent on what data is included.

Another possible cause of the low correlations found in this model-bound analysis is the simplicity of the design matrices. The simple designs may not be able to accurately model the very complex nature of the movement into the New World. A last cause could be that most of the connection schemes combine all the geographic Paleoamerican groupings into one box, which in actuality combines them into one big group. As was shown in the principal component analyses, there are distinct differences between the groupings of Paleoamericans. All of the previously proposed migration scenarios refer to Paleoamericans as a whole, not geographic Paleoamerican groupings. Thus, there may need to be changes in the previously proposed models of migration or the development of a new theory in order to account for the differences found between Paleoamericans on different continents.

Chapter Seven: Conclusion

The results presented here lend support to several models or hypotheses put forth by previous researchers focusing on the peopling of the New World. Although the focus of this dissertation was to test previously proposed hypotheses regarding migration scenarios and ancestral areas, two ancillary conclusions need to be mentioned. First, the Paleoamerican groupings are not more internally variable in terms of cranial metrics than other Archaic or modern, worldwide samples. This finding is at odds with those reported by Powell and Neves (1999), which has been cited often. This may be the result of different samples and statistical procedures used in this study from those in Powell and Neves (1999).

Additionally, there is a clear separation/difference between the North and South American Paleoamerican cranial phenotypes. Central American Paleoamericans also do not appear to be intermediaries between the two subsets. This could be an indication of genotypic dissimilarity between individuals inhabiting these geographically separated areas or intense in situ evolution from one ancestral population. This can be construed as evidence for the Recurrent Gene Flow model of migration into the New World, which posits that there was a single wave of movement into the Americas by a highly diverse (both phenotypically and genotypically) population.

However, the majority of evidence presented here supports a Single Wave model of movement into the New World. The model-bound analysis involving design matrices only found significant correlation with one of the variants of the

Single Wave design. This design matrix modeled one of the two recurring observations of genetic evidence: a single ancestor group from Northeast Asia (represented here by the modern Buriat population) moved into the New World in one wave after being confined in Beringia (referred to as the Beringian Standstill) during the Late Pleistocene (Bonatto and Salzano, 1997 a; Fagundes et al., 2007 a,b; Tamm et al., 2007).

Additional evidence of the Single Wave model presented in this dissertation is the phenotypic similarities between the Paleoamerican, Archaic and modern populations from similar geographic areas. This is shown in both the principal component analyses and Mahalanobis distances. This argues for phenotypic continuity between temporally-different American populations and against a complete replacement of the earliest Americans by another wave of craniometrically different populations as argued by proponents of the Two Components model.

Thus, the results of the analysis do not lend support to the dissertation's first hypothesis: the Two Components model provides the best explanation of movement into the New World. This dissertation provides more evidence supporting the Single Wave migration model. This is an important finding, because, while genetic evidence has supported the Single Wave model for years, craniometric evidence has not, generally favoring the Two Component model. Therefore, with the results presented here, there is craniometric support, in addition to genetic support, for the Single Wave model. The Single Wave and Recurrent Gene Flow models have many similarities and a clearer description of

the Recurrent Gene Flow model is needed in order to make clearer distinctions between the two.

The second focus of this dissertation was to ascertain a clear picture regarding the possible ancestral area(s)/ origination point(s) of the Paleoamericans. The results provided by the various statistical procedures do not provide a clear-cut answer; however, several trends arise. First, all Paleoamerican groupings have notable phenotypic similarities with certain Southeast Asian/Polynesian populations as well as eastern Asian populations. If all Paleoamerican populations are the result of a single wave, then these areas are good contenders for the origination point of this wave. This provides some support for the hypothesis put forth at the beginning of the dissertation that evidence would suggest southern Asia or the Pacific Rim as the ancestral area for the Paleoamericans.

However, similarities between different areas and Paleoamerican groupings are also evidenced here. The first is that, with the North American Paleoamericans, there is a consistent connection with European populations. This is particularly evident in the individual Paleoamerican Mahalanobis squared distance results but also present in the other forms of analysis.

This phenotypic similarity could be the result of two causes. Genotypic similarities with Europeans and the first Americans could cause phenotypic similarities, arguing that at least some of the Paleoamericans had European ancestors. Secondly, the phenotypic similarities could be the result of similar adaptations causing similar craniometric traits. A better understanding of the

plasticity of the cranium is needed to better understand this connection. A similar scenario is also present with the South American Paleoamericans but instead of phenotypic similarity with European populations, there are notable craniometric similarities with African populations. The same explanations provided above could account for these similarities. Thus, there is not a clear picture provided by the results of this analysis in terms of ancestral areas of the first Americans.

Future directions of research include the addition of similarly dated Old World samples to the Paleoamericans and Archaic Americans. While not comparable to many previous studies, which utilize the Howells' samples, it could provide a clearer and more accurate picture of ancestral area(s) and migration routes. In addition, the development of a migration scenario that can adequately account for the phenotypic differences in Paleoamericans from different continents is needed. Although these results support the Single Wave model, this hypothesis does not explain the phenotypic differences between Paleoamericans on different continents.

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Appendices

Appendix A

Table 1: Single Wave 1 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	0																								
2	0	0																							
3	0	0	0																						
4	0	0	0	0																					
5	0	0	0	0	0																				
6	0	0	0	0	0	0																			
7	0	0	0	0	0	0	0																		
8	0	0	0	0	0	0	0	0																	
9	0	0	0	0	0	0	0	0	0																
10	0	0	0	0	0	0	0	0	0	0															
11	1	1	1	1	1	1	1	1	1	1	0														
12	1	1	1	1	1	1	1	1	1	1	0	0													
13	1	1	1	1	1	1	1	1	1	1	0	0	0												
14	1	1	1	1	1	1	1	1	1	1	0	0	0	0											
15	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0										
16	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0									
17	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0								
18	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0							
19	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0						
20	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0					
21	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0				
22	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0			
23	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0		
24	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	
25	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

1: Ainu; 2: Andaman; 3: Atayal; 4: Easter; 5: Guam; 6: Maori; 7: Mokapu; 8: Moriori; 9: Philippines; 10: Tolai; 11: Anyang; 12: Buriat; 13: Hainan; 14: North Japan; 15: South Japan; 16: Arikara; 17: Brazilian Archaic; 18:Central American Paleo; 19: Colombian Archaic; 20: Midwest North American Archaic; 21: North American Paleo; 22: Peru; 23: Santa Cruz; 24: South American Paleo; 25: Southeast North American Archaic

Table 21: Single Wave 2 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	0																								
2	0	0																							
3	0	0	0																						
4	0	0	0	0																					
5	0	0	0	0	0																				
6	0	0	0	0	0	0																			
7	0	0	0	0	0	0	0																		
8	0	0	0	0	0	0	0	0																	
9	0	0	0	0	0	0	0	0	0																
10	0	0	0	0	0	0	0	0	0	0															
11	1	1	1	1	1	1	1	1	1	1	0														
12	1	1	1	1	1	1	1	1	1	1	0	0													
13	1	1	1	1	1	1	1	1	1	1	0	0	0												
14	1	1	1	1	1	1	1	1	1	1	0	0	0	0											
15	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0										
16	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0									
17	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0								
18	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0							
19	3	3	3	3	3	3	3	3	3	3	2	2	2	2	2	1	1	1	0						
20	3	3	3	3	3	3	3	3	3	3	2	2	2	2	2	1	1	1	0	0					
21	3	3	3	3	3	3	3	3	3	3	2	2	2	2	2	1	1	1	0	0	0				
22	3	3	3	3	3	3	3	3	3	3	2	2	2	2	2	1	1	1	0	0	0	0			
23	4	4	4	4	4	4	4	4	4	4	3	3	3	3	3	2	2	2	1	1	1	1	0		
24	4	4	4	4	4	4	4	4	4	4	3	3	3	3	3	2	2	2	1	1	1	1	0	0	
25	4	4	4	4	4	4	4	4	4	4	3	3	3	3	3	2	2	2	1	1	1	1	0	0	0

1: Ainu; 2: Andaman; 3: Atayal; 4: Easter; 5: Guam; 6: Maori; 7: Mokapu; 8: Moriori; 9: Philippines: 10: Tolai; 11: Anyang; 12: Buriat; 13: Hainan; 14: North Japan; 15: South Japan; 16: Central American Paleo; 17: North American Paleo; 18: South American Paleo; 19: Brazilian Archaic; 20: Colombian Archaic; 21: Midwest North American Archaic; 22: Southeast North American Archaic; 23: Arikara; 24: Peru; 25: Santa Cruz

Table 22: Single Wave 3 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11
1	0										
2	2	0									
3	2	0	0								
4	2	0	0	0							
5	2	0	0	0	0						
6	2	0	0	0	0	0					
7	2	0	0	0	0	0	0				
8	2	0	0	0	0	0	0	0			
9	2	0	0	0	0	0	0	0	0		
10	2	0	0	0	0	0	0	0	0	0	
11	2	0	0	0	0	0	0	0	0	0	0

1: Buriat; 2: Arikara; 3: Brazilian Archaic; 4: Central American Paleo; 5: Colombian Archaic; 6: Midwest North American Archaic; 7: North American Paleo; 8: Peru; 9: Santa Cruz; 10: South American Paleo; 11: Southeast North American Archaic

Table 23: Single Wave 4 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	0														
2	0	0													
3	0	0	0												
4	0	0	0	0											
5	0	0	0	0	0										
6	2	2	2	2	2	0									
7	2	2	2	2	2	0	0								
8	2	2	2	2	2	0	0	0							
9	2	2	2	2	2	0	0	0	0						
10	2	2	2	2	2	0	0	0	0	0					
11	2	2	2	2	2	0	0	0	0	0	0				
12	2	2	2	2	2	0	0	0	0	0	0	0			
13	2	2	2	2	2	0	0	0	0	0	0	0	0		
14	2	2	2	2	2	0	0	0	0	0	0	0	0	0	
15	2	2	2	2	2	0	0	0	0	0	0	0	0	0	0

1: Ainu; 2: Atayal; 3: Hainan; 4: North Japan; 5: South Japan; 6: Arikara; 7: Brazilian Archaic; 8: Central American Paleo; 9: Colombian Archaic; 10: Midwest North American Archaic; 11: North American Paleo; 12: Peru; 13: Santa Cruz; 14: South American Paleo; 15: Southeast North American Archaic

Table 24: Two Components 1 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0																	
2	0	0																
3	0	0	0															
4	1	1	1	0														
5	1	1	1	0	0													
6	1	1	1	0	0	0												
7	1	1	1	0	0	0	0											
8	2	2	2	2	2	2	2	0										
9	2	2	2	2	2	2	2	0	0									
10	2	2	2	2	2	2	2	0	0	0								
11	3	3	3	3	3	3	3	1	1	1	0							
12	3	3	3	3	3	3	3	1	1	1	0	0						
13	3	3	3	3	3	3	3	1	1	1	0	0	0					
14	3	3	3	3	3	3	3	1	1	1	0	0	0	0				
15	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0			
16	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0		
17	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0	0	
18	3.5	3.5	3.5	3.5	3.5	3.5	3.5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Midwest North American Archaic; 5: Southeast North American Archaic; 6: Brazilian Archaic; 7: Colombian Archaic; 8: Arikara; 9: Santa Cruz; 10: Peru; 11: Ainu; 12: Atayal; 13: Anyang; 14: Hainan; 15: Buriat; 16: North Japan; 17: South Japan; 18: Eskimo

Table 25: Two Components 2 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0																	
2	0	0																
3	0	0	0															
4	2	2	2	0														
5	2	2	2	0	0													
6	2	2	2	0	0	0												
7	2	2	2	0	0	0	0											
8	2	2	2	2	2	2	2	0										
9	2	2	2	2	2	2	2	0	0									
10	2	2	2	2	2	2	2	0	0	0								
11	3	3	3	3	3	3	3	1	1	1	0							
12	3	3	3	3	3	3	3	1	1	1	0	0						
13	3	3	3	3	3	3	3	1	1	1	0	0	0					
14	3	3	3	3	3	3	3	1	1	1	0	0	0	0				
15	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0			
16	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0		
17	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0	0	
18	2.5	2.5	2.5	2.5	2.5	2.5	2.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Midwest North American Archaic; 5: Southeast North American Archaic; 6: Brazilian Archaic; 7: Colombian Archaic; 8: Arikara; 9: Santa Cruz; 10: Peru; 11: Ainu; 12: Atayal; 13: Anyang; 14: Hainan; 15: Buriat; 16: North Japan; 17: South Japan; 18: Eskimo

Table 26: Two Components 3 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0																	
2	0	0																
3	0	0	0															
4	2	2	2	0														
5	2	2	2	0	0													
6	2	2	2	0	0	0												
7	2	2	2	0	0	0	0											
8	2	2	2	2	2	2	2	0										
9	2	2	2	2	2	2	2	0	0									
10	2	2	2	2	2	2	2	0	0	0								
11	3	3	3	3	3	3	3	1	1	1	0							
12	3	3	3	3	3	3	3	1	1	1	0	0						
13	3	3	3	3	3	3	3	1	1	1	0	0	0					
14	3	3	3	3	3	3	3	1	1	1	0	0	0	0				
15	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0			
16	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0		
17	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0	0	
18	3.5	3.5	3.5	3.5	3.5	3.5	3.5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Midwest North American Archaic; 5: Southeast North American Archaic; 6: Brazilian Archaic; 7: Colombian Archaic; 8: Arikara; 9: Santa Cruz; 10: Peru; 11: Ainu; 12: Atayal; 13: Anyang; 14: Hainan; 15: Buriat; 16: North Japan; 17: South Japan; 18: Eskimo

Table 27: Two Components 4 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	0																
2	0	0															
3	0	0	0														
4	0	0	0	0													
5	0	0	0	0	0												
6	0	0	0	0	0	0											
7	0	0	0	0	0	0	0										
8	2	2	2	2	2	2	2	0									
9	2	2	2	2	2	2	2	0	0								
10	2	2	2	2	2	2	2	0	0	0							
11	3	3	3	3	3	3	3	1	1	1	0						
12	3	3	3	3	3	3	3	1	1	1	0	0					
13	3	3	3	3	3	3	3	1	1	1	0	0	0				
14	3	3	3	3	3	3	3	1	1	1	0	0	0	0			
15	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0		
16	3	3	3	3	3	3	3	1	1	1	0	0	0	0	0	0	
17	3.5	3.5	3.5	3.5	3.5	3.5	3 .5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Midwest North American Archaic; 5: Southeast North American Archaic; 6: Brazilian Archaic; 7: Colombian Archaic; 8: Arikara; 9: Santa Cruz; 10: Peru; 11: Ainu; 12: Atayal; 13: Hainan; 14: Buriat; 15: North Japan; 16: South Japan; 17: Eskimo

Table 28: Two Components 5 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	0																				
2	0	0																			
3	0	0	0																		
4	1	1	1	0																	
5	1	1	1	0	0																
6	1	1	1	0	0	0															
7	1	1	1	0	0	0	0														
8	1	1	1	0	0	0	0	0													
9	1	1	1	0	0	0	0	0	0												
10	1	1	1	0	0	0	0	0	0	0											
11	1	1	1	0	0	0	0	0	0	0	0										
12	1	1	1	0	0	0	0	0	0	0	0	0									
13	1	1	1	0	0	0	0	0	0	0	0	0	0								
14	2	2	2	1	1	1	1	1	1	1	1	1	1	0							
15	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0						
16	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0					
17	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0	0				
18	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0			
19	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0		
20	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	
21	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Ainu; 5: Andaman; 6: Atayal; 7: Easter Island; 8: Guam; 9: Maori; 10: Mokapu; 11: Moriori; 12: Philippines; 13: Tolai; 14: Anyang; 15: Buriat; 16: Hainan; 17: North Japan; 18: South Japan; 19: Arikara; 20: Peru; 21: Santa Cruz

Table 29: Two Components 6 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	0																								
2	0	0																							
3	0	0	0																						
4	0	0	0	0																					
5	0	0	0	0	0																				
6	0	0	0	0	0	0																			
7	0	0	0	0	0	0	0																		
8	1	1	1	1	1	1	1	0																	
9	1	1	1	1	1	1	1	0	0																
10	1	1	1	1	1	1	1	0	0	0															
11	1	1	1	1	1	1	1	0	0	0	0														
12	1	1	1	1	1	1	1	0	0	0	0	0													
13	1	1	1	1	1	1	1	0	0	0	0	0	0												
14	1	1	1	1	1	1	1	0	0	0	0	0	0	0											
15	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0										
16	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0									
17	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0								
18	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	0							
19	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0						
20	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0					
21	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0	0				
22	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0			
23	3	3	3	3	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0		
24	3	3	3	3	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	
25	3	3	3	3	3	3	3	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0

1: North American Paleo; 2: Central American Paleo; 3: South American Paleo; 4: Midwest North American Archaic; 5: Southeast North American Archaic; 6: Brazilian Archaic; 7: Colombian Archaic; 8: Ainu; 9: Andaman Islands; 10: Atayal; 11: Easter Island; 12: Guam; 13: Maori; 14: Mokapu; 15: Moriori; 16: Philippines; 17: Tolai; 18: Anyang; 19: Buriat; 20: Hainan; 21: North Japan; 22: South Japan; 23: Arikara; 24: Peru; 25: Santa Cruz

Table 30: Two Components 7 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	0																								
2	0	0																							
3	0	0	0																						
4	0	0	0	0																					
5	0	0	0	0	0																				
6	0	0	0	0	0	0																			
7	0	0	0	0	0	0	0																		
8	0	0	0	0	0	0	0	0																	
9	0	0	0	0	0	0	0	0	0																
10	0	0	0	0	0	0	0	0	0	0															
11	1	1	1	1	1	1	1	1	1	1	0														
12	1	1	1	1	1	1	1	1	1	1	0	0													
13	1	1	1	1	1	1	1	1	1	1	0	0	0												
14	1	1	1	1	1	1	1	1	1	1	0	0	0	0											
15	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0										
16	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0									
17	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0								
18	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0							
19	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0	0						
20	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0	0	0					
21	1	1	1	1	1	1	1	1	1	1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1	1	1	0				
22	1	1	1	1	1	1	1	1	1	1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1	1	1	0	0			
23	1	1	1	1	1	1	1	1	1	1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1	1	1	0	0	0		
24	1	1	1	1	1	1	1	1	1	1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1	1	1	0	0	0	0	
25	1	1	1	1	1	1	1	1	1	1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1	1	1	0	0	0	0	0

1: Ainu; 2: Andaman Islands; 3: Atayal; 4: Easter Island; 5: Guam; 6: Maori; 7: Mokapu; 8: Moriori; 9: Philippines; 10: Tolai; 11: North American Paleo; 12: Central American Paleo; 13: South American Paleo; 14: Midwest North American Archaic; 15: Southeast North American Archaic; 16: Brazilian Archaic; 17: Colombian Archaic; 18: Arikara; 19: Peru; 20: Santa Cruz; 21: Anyang; 22: Buriat; 23: Hainan; 24: North Japan; 25: South Japan

Table 31: Three Waves Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	0																									
2	0	0																								
3	0	0	0																							
4	0	0	0	0																						
5	0	0	0	0	0																					
6	0	0	0	0	0	0																				
7	0	0	0	0	0	0	0																			
8	0	0	0	0	0	0	0	0																		
9	0	0	0	0	0	0	0	0	0																	
10	0	0	0	0	0	0	0	0	0	0																
11	1	1	1	1	1	1	1	1	1	1	0															
12	1	1	1	1	1	1	1	1	1	1	0	0														
13	1	1	1	1	1	1	1	1	1	1	0	0	0													
14	1	1	1	1	1	1	1	1	1	1	0	0	0	0												
15	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0											
16	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0										
17	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0									
18	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0								
19	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0							
20	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0						
21	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0					
22	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0				
23	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0			
24	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0		
25	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	
26	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	0

1: Ainu; 2: Andaman Islands; 3: Atayal; 4: Easter Island; 5: Guam; 6: Maori; 7: Mokapu; 8: Moriori; 9: Philippines; 10: Tolai; 11: Anyang; 12: Buriat; 13: Hainan; 14: North Japan; 15: South Japan; 16: Arikara; 17: Peru; 18: Santa Cruz; 19: North American Paleo; 20: Central American Paleo; 21: South American Paleo; 22: Midwest North American Archaic; 23: Southeast North American Archaic; 24: Brazilian Archaic; 25: Colombian Archaic; 26: Eskimo

Table 32: Recurrent Gene Flow 1 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	0																									
2	0	0																								
3	0	0	0																							
4	0	0	0	0																						
5	0	0	0	0	0																					
6	0	0	0	0	0	0																				
7	0	0	0	0	0	0	0																			
8	0	0	0	0	0	0	0	0																		
9	0	0	0	0	0	0	0	0	0																	
10	0	0	0	0	0	0	0	0	0	0																
11	0	0	0	0	0	0	0	0	0	0	0															
12	0	0	0	0	0	0	0	0	0	0	0	0														
13	0	0	0	0	0	0	0	0	0	0	0	0	0													
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0											
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0										
17	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0									
18	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0	0								
19	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0	0	0							
20	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2	0						
21	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2	0	0					
22	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2	0	0	0				
23	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2	0	0	0	0			
24	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	3	3	3	1	1	1	1	0		
25	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	3	3	3	1	1	1	1	0	0	
26	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	3	3	3	1	1	1	1	0	0	0

1: Ainu; 2: Andaman Island; 3: Anyang; 4: Atayal; 5: Easter Island; 6: Guam; 7: Hainan; 8: Maori; 9: Mokapu; 10: Moriori; 11: North Japan; 12: Philippines; 13: South Japan; 14: Tolai; 15: Buriat; 16: Eskimo; 17: North American Paleo; 18: Central American Paleo; 19: South American Paleo; 20: Midwest North American Archaic; 21: Southeast North American Archaic; 22: Brazilian Archaic; 23: Colombian Archaic; 24: Arikara; 25: Peru; 26: Santa Cruz

Table 33: Recurrent Gene Flow 2 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	0																									
2	0	0																								
3	0	0	0																							
4	0	0	0	0																						
5	0	0	0	0	0																					
6	0	0	0	0	0	0																				
7	0	0	0	0	0	0	0																			
8	0	0	0	0	0	0	0	0																		
9	0	0	0	0	0	0	0	0	0																	
10	0	0	0	0	0	0	0	0	0	0																
11	0	0	0	0	0	0	0	0	0	0	0															
12	0	0	0	0	0	0	0	0	0	0	0	0														
13	0	0	0	0	0	0	0	0	0	0	0	0	0													
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0											
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0										
17	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0									
18	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0	0								
19	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0	0	0							
20	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	0	0	0	0						
21	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	1	1	1	1	0					
22	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	1	1	1	1	0	0				
23	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	1	1	1	1	0	0	0			
24	3	3	3	3	3	3	3	3	3	3	3	3	3	3	4	4	5	5	5	5	6	6	6	0		
25	3	3	3	3	3	3	3	3	3	3	3	3	3	3	4	4	5	5	5	5	6	6	6	0	0	
26	3	3	3	3	3	3	3	3	3	3	3	3	3	3	4	4	5	5	5	5	6	6	6	0	0	0

1: Ainu; 2: Andaman Islands; 3: Anyang; 4: Atayal; 5: Easter Island; 6: Guam; 7: Hainan; 8: Maori; 9: Mokapu; 10: Moriori; 11: North Japan; 12: Philippines; 13: South Japan; 14: Tolai; 15: Buriat; 16: Eskimo; 17: Midwest North American Archaic; 18: Southeast North American Archaic; 19: Brazilian Archaic; 20: Colombian Archaic; 21: Arikara; 22: Peru; 23: Santa Cruz; 24: North American Paleo; 25: Central American Paleo; 26: South American Paleo

Table 34: Recurrent Gene Flow 3 Design Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	0																									
2	0	0																								
3	0	0	0																							
4	0	0	0	0																						
5	0	0	0	0	0																					
6	0	0	0	0	0	0																				
7	0	0	0	0	0	0	0																			
8	0	0	0	0	0	0	0	0																		
9	0	0	0	0	0	0	0	0	0																	
10	0	0	0	0	0	0	0	0	0	0																
11	0	0	0	0	0	0	0	0	0	0	0															
12	0	0	0	0	0	0	0	0	0	0	0	0														
13	0	0	0	0	0	0	0	0	0	0	0	0	0													
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
15	2	2	2	2	2	2	2	2	2	2	2	2	2	2	0											
16	2	2	2	2	2	2	2	2	2	2	2	2	2	2	0	0										
17	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	0									
18	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	0	0								
19	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	0	0	0							
20	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	0	0	0	0						
21	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	4	4	4	4	0					
22	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	4	4	4	4	0	0				
23	4	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	4	4	4	4	0	0	0			
24	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	3	3	3	0		
25	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	3	3	3	0	0	
26	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	3	3	3	0	0	0

1: Ainu3; 2: Andaman Islands; 3: Anyang; 4: Atayal; 5: Easter Island; 6: Guam; 7: Hainan; 8: Maori; 9: Mo1kapu; 10: Moriori; 11: North Japan; 12: Philippines; 13: South Japan; 14: Tolai; 15: Buriat; 16: Eskimo; 17: Midwest North American Archaic; 18: Southeast North American Archaic; 19: Brazilian Archaic; 20: Colombian Archaic; 21: Arikara; 22: Peru; 23: Santa Cruz; 24: North American Paleo; 25: Central American Paleo; 26: South American Paleo

Appendix B

Table 35: Means and Standard Deviations for All Population

Location	Statistics	Principal Component One	Principal Component Two
Africa/ Modern	Mean	-1.1378527	1.4191158
Africa/ Modern	Standard Deviation	2.1474810	1.1400550
Australia/ Modern	Mean	-0.2241430	1.1880656
Australia/ Modern	Standard Deviation	2.1915508	1.0114253
Brazil/ Archaic	Mean	-0.3171788	0.6250057
Brazil/ Archaic	Standard Deviation	1.8711056	0.7794898
Central America/ Paleo	Mean	2.5283101	0.1565432
Central America/ Paleo	Standard Deviation	1.1508000	0.9106458
E. Asia/ Modern	Mean	0.2608306	-0.0311388
E. Asia/ Modern	Standard Deviation	2.2272419	1.1141579
Colombia/ Archaic	Mean	-0.1153654	0.7901036
Colombia/ Archaic	Standard Deviation	1.7276472	1.2928221
Europe/ Modern	Mean	0.8215425	-0.0461623
Europe/ Modern	Standard Deviation	2.1084848	1.1883647
MW North America/ Archaic	Mean	0.0900197	-0.8687101
MW North America/ Archaic	Standard Deviation	2.0877547	1.1178968
Melanesia/ Modern	Mean	-0.9681793	1.3754553
Melanesia/ Modern	Standard Deviation	1.8916328	0.9145754
Micronesia/ Modern	Mean	1.4730774	1.4730774
Micronesia/ Modern	Standard Deviation	2.0395856	1.0368725
North America/ Modern	Mean	-0.3096319	-1.5049212
North America/ Modern	Standard Deviation	2.0859658	1.0015715
North America/ Paleo	Mean	0.5441969	-1.1959015

Table 35 continued: Means and Standard Deviations for All Population

Location	Statistics	Principal Component One	Principal Component Two
North America/ Paleo	Standard Deviation	1.8666683	1.3847943
Northeast Asia/ Modern	Mean	2.2601458	-3.1612067
Northeast Asia/ Modern	Standard Deviation	2.3324120	1.0522744
Northern North America/ Modern	Mean	0.7234921	-0.2123843
Northern North America/ Modern	Standard Deviation	1.7097906	0.9470042
Polynesia/ Modern	Mean	0.8975785	-0.4663305
Polynesia/ Modern	Standard Deviation	2.3106036	1.3692902
South America/ Modern	Mean	-1.2493157	-1.2397457
South America/ Modern	Standard Deviation	1.9878635	1.2015927
South America/ Paleo	Mean	-0.6241026	0.6403708
South America/ Paleo	Standard Deviation	2.0343505	1.3357209
SE Asia/ Modern	Mean	-1.7765655	0.1613763
SEAsia/ Modern	Standard Deviation	2.6993460	1.0907221
SE North America/ Archaic	Mean	0.3247209	-0.5518397
SE North America/ Archaic	Standard Deviation	2.1009187	0.8684220
	F-test (P-value)	3.06 (0.0010***)	3.17 (0.0007***)

***** Significant at a 0.05 level**

Appendix C

Table 36: Full Biological Distance Matrix

	Ainu	Andaman	Anyang	Arikara	Atayal	Australia	Brazilian Archaic	Berg	Buriat	Bushman	Colombia Archaic	Central America Paleo	Dogon
Ainu	0.000												
Andaman	16.112	0.000											
Anyang	9.933	18.250	0.000										
Arikara	12.554	18.049	12.376	0.000									
Atayal	9.315	11.685	8.317	13.336	0.000								
Australia	12.715	25.852	25.354	27.581	16.148	0.000							
Brazilian Archaic	7.682	12.423	7.712	13.509	4.359	8.495	0.000						
Berg	9.361	15.400	18.658	12.933	12.536	26.675	14.534	0.000					
Buriat	19.619	34.112	18.233	14.917	27.997	52.835	29.598	15.947	0.000				
Bushman	11.714	15.769	21.193	33.463	14.626	12.468	12.304	20.960	45.569	0.000			
Colombia Archaic	5.345	10.189	6.909	14.668	5.691	9.348	2.387	16.458	28.936	9.817	0.000		
Central America Paleo	13.890	24.979	16.550	15.619	19.092	23.116	13.615	26.576	30.843	32.519	9.430	0.000	
Dogon	12.078	7.891	17.369	26.841	12.236	19.343	9.469	19.122	39.222	8.839	6.568	19.221	0.000

Table 36 continued: Full Biological Distance Matrix

	Ainu	Andaman	Anyang	Arikara	Atayal	Australia	Brazilian Archaic	Berg	Buriat	Bushman	Colombia Archaic	Central America Paleo	Dogon
Easter	11.734	20.692	12.280	18.513	11.577	9.671	6.375	22.937	38.325	18.834	5.979	13.287	20.651
Eskimo	11.228	31.752	14.359	17.825	17.525	17.303	14.112	29.982	30.217	26.940	13.534	22.785	30.764
Guam	8.450	18.189	5.148	9.796	8.213	20.629	7.507	15.984	18.648	20.910	6.909	13.271	16.740
Hainan	9.280	9.364	3.207	9.072	6.660	24.706	6.210	13.308	17.409	19.477	5.450	14.339	11.048
Maori	10.756	24.913	13.757	9.866	13.927	15.065	10.292	19.885	23.394	27.579	9.672	10.097	25.831
Midwest NA Archaic	5.571	11.804	10.363	7.144	14.578	22.310	12.621	11.683	15.222	18.597	8.820	14.986	15.927
Mokapu	11.929	16.362	10.342	9.116	15.235	22.793	11.452	18.617	19.274	26.550	7.802	7.540	20.367
Moriori	12.483	19.421	15.102	5.762	17.959	22.687	14.526	21.301	21.450	32.645	10.928	7.017	24.420
North American Paleo	11.305	21.697	17.292	6.628	19.234	29.574	18.072	10.347	14.908	32.267	19.648	26.278	30.740
North Japan	3.153	10.875	5.758	9.263	4.814	15.351	4.622	11.011	16.542	14.909	3.060	11.031	10.872
Norse	3.357	13.881	12.562	10.511	11.650	16.633	10.351	7.704	23.002	15.537	8.379	16.010	13.807
Peru	9.202	12.145	9.366	4.295	8.662	23.325	9.357	11.128	15.693	24.076	8.806	13.615	18.913
Phillipines	7.013	7.459	4.928	9.095	5.305	18.514	4.681	9.670	19.412	15.279	4.258	14.045	8.343

Table 36 continued: Full Biological Distance Matrix

	Ainu	Andaman	Anyang	Arikara	Atayal	Australia	Brazilian Archaic	Berg	Buriat	Bushman	Colombia Archaic	Central America Paleo	Dogon
Santa Cruz	8.773	12.382	13.273	5.888	10.451	16.661	9.222	11.033	18.559	19.948	9.375	15.984	18.590
South American Paleo	5.945	10.816	9.009	16.208	4.055	9.139	3.125	13.336	29.450	6.590	2.459	16.755	7.678
South Japan	4.304	9.597	4.490	9.565	3.240	17.508	4.829	11.912	20.418	14.427	3.255	12.829	9.295
Southeast North American Archaic	5.034	14.700	8.735	7.008	6.394	13.953	5.608	8.894	19.138	16.075	6.900	16.704	15.588
Tasmania	14.922	21.569	23.696	25.083	15.226	6.112	9.920	20.466	45.277	14.166	11.398	28.619	21.458
Teita	12.368	15.313	17.456	26.090	11.521	13.484	9.333	22.393	49.212	7.913	9.120	25.037	9.152
Tolai	11.270	17.353	14.800	18.857	9.897	4.365	3.699	22.203	42.108	12.741	5.588	20.699	15.634
Zalavar	3.714	14.575	12.940	11.878	8.850	14.486	8.743	4.866	22.752	13.036	8.693	20.990	15.609
Zulu	8.532	17.890	20.043	27.174	14.323	11.324	10.057	20.323	45.559	7.009	7.578	18.355	7.036

Table 36 continued: Full Biological Distance Matrix

	Easter	Eskimo	Guam	Hainan	Maori	Midwest North American Archaic	Mokapu	Moriori	North American Paleo	North Japan	Norse	Peru	Phillipines
Easter	0.000												
Eskimo	13.131	0.000											
Guam	10.631	9.427	0.000										
Hainan	13.135	16.801	5.106	0.000									
Maori	8.250	10.115	7.235	13.927	0.000								
Midwest North American Archaic	15.850	16.453	8.859	7.597	11.254	0.000							
Mokapu	11.837	18.168	9.616	8.348	6.912	7.779	0.000						
Moriori	13.396	15.946	10.509	11.915	4.853	7.234	4.823	0.000					
North American Paleo	22.918	21.719	19.516	14.255	16.670	8.967	16.081	13.685	0.000				
North Japan	9.768	11.913	6.213	4.423	8.581	5.873	7.637	9.095	11.735	0.000			
Norse	12.636	17.397	11.338	9.423	13.314	6.327	13.254	11.676	7.943	7.160	0.000		
Peru	13.742	16.553	10.364	5.341	10.822	7.989	6.049	7.284	7.024	4.838	7.753	0.000	
Phillipines	13.162	19.020	6.080	3.048	12.756	6.960	8.806	11.915	14.528	3.785	7.731	7.172	0.000

Table 36 continued: Full Biological Distance Matrix

	Easter	Eskimo	Guam	Hainan	Maori	Midwest North American Archaic	Mokapu	Moriori	North American Paleo	North Japan	Norse	Peru	Phillipines
Santa Cruz	13.166	16.449	10.713	10.854	8.227	7.107	9.913	6.866	9.886	5.673	8.861	5.661	6.938
South American Paleo	8.406	13.419	5.758	7.365	11.903	10.817	12.879	16.347	22.380	4.912	9.726	11.579	4.921
South Japan	10.043	11.852	4.840	2.500	11.152	6.958	10.067	11.004	13.194	1.574	5.838	5.194	3.363
Southeast North American Archaic	13.158	12.143	7.719	7.623	9.264	8.953	9.516	11.485	8.989	4.807	5.869	4.582	4.931
Tasmania	14.144	26.014	21.740	22.515	17.056	18.978	20.859	24.446	25.800	16.045	18.441	23.102	15.766
Teita	13.483	23.581	15.698	15.494	25.875	18.629	27.579	27.732	30.743	14.466	12.334	21.761	12.661
Tolai	8.659	14.689	13.987	13.418	15.175	16.770	16.998	19.175	23.341	10.468	14.439	15.419	10.795
Zalavar	13.007	18.162	11.754	10.382	14.002	8.125	13.786	16.344	8.662	7.318	2.753	8.516	7.985
Zulu	16.311	24.270	17.608	17.247	23.750	17.498	21.085	25.801	30.096	13.287	11.200	20.251	13.300

Table 36 continued: Full Biological Distance Matrix

	Santa Cruz	South American Paleo	South Japan	Southeast North American Archaic	Tasmania	Teita	Tolai	Zalavar	Zulu
Santa Cruz	0.000								
South American Paleo	9.534	0.000							
South Japan	8.306	4.415	0.000						
Southeast North American Archaic	5.824	6.499	5.121	0.000					
Tasmania	17.439	10.584	18.953	14.805	0.000				
Teita	18.506	6.792	10.484	15.812	20.170	0.000			
Tolai	13.837	5.601	10.965	9.624	6.137	10.992	0.000		
Zalavar	10.623	7.824	6.906	4.357	11.854	14.125	11.617	0.000	
Zulu	20.724	7.456	11.890	12.772	17.762	6.162	11.446	11.062	0.000

Vita

B. Kathleen Alsup was born Barbara Kathleen Thompson in Rantoul, IL on March 25, 1983. She is the daughter of Greg and Donna Thompson. Kathleen attended the University of Tennessee starting in 2001, received her Bachelor of Arts in 2005 and her Master of Arts in 2007. She married James Alsup in May 2006 and welcomed her children, Ethan Alsup in May 2009 and Harper Alsup in February 2012. She began her doctoral work in August 2007 and received her Doctorate in Philosophy in December 2012.